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Appl. No. 10/718,264
Atty. Dkt. No. 042049-0105

Remarks

Disposition of the claims

Claims 17-28 are pending and stand rejected. Claims 1-2 were canceled without prejudice or disclaimer before this amendment was filed. Claims 3-16 were withdrawn. Claims 29-86 are new.

Claims 17 and 23 are currently amended. Support for these amendments may be found throughout the Specification, and at least at paragraph 53 and in the fourth row of the table below. Accordingly, no new matter has been added.

Claim 29 serves as the base claim for claims 30-40. Claims 75-86 recite a method of use. Support for these amendments may be found throughout the Specification, and at least the exemplary passages in the table below. Accordingly, as to these claims, no new matter has been added.

Claim	specification
29. (New) A vaccine comprising, in an acceptable pharmaceutical vehicle, a nucleic acid having a nucleotide sequence with at least 90% sequence identity to SEQ ID No. 15,	The present invention relates to vaccines comprising a nucleotide sequence ... selected from SEQ ID No. 15 (para. 15). Homologous nucleotide sequence in the sense of the present invention is understood as meaning a nucleotide sequence having at least a percentage identity with the bases of a nucleotide sequence according to the invention of ... preferably 90% or 95% (para. 57).
wherein said nucleic acid encodes an immunogenic protein that induces a protective response effective against infection by a piglet weight loss disease circovirus,	Examples 5-8.
wherein said nucleotide	[A]lternatively the sequences SEQ ID No. 23 (ORF'1),

sequence comprises a sequence having at least 90% sequence identity to at least one of SEQ ID No. 23 and SEQ ID No. 25.	SEQ ID No. 25 (ORF'2) and SEQ ID No. 27 (ORF'3), respectively corresponding to the sequences between the positions 51 and 995 determined with respect to the position of the nucleotides on the sequence SEQ ID No. 15, the positions 1734 and 1033 and the positions 670 and 357, the positions being determined with respect to the position of the nucleotides on the sequence SEQ ID No. 19 (represented according to the orientation 3'→5'), the ends being included, are finally preferred. (Para. 75). As far as homology with the nucleotide sequence[] ... SEQ ID No. 25 ...is concerned, the homologous ... 90% or 95% ... are preferred. (para. 81).
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Claim 41 is analogous to claim 29 but recites 95% (instead of 90%) sequence identity to *at least one of SEQ ID No. 23 and SEQ ID No. 25*. Claim 41 serves as a base for claims 42-51, and claims 64-74 recite a method of use. Support for these amendments may be found throughout the Specification, and at least at the passages quoted in the table above. Accordingly, as to these claims, no new matter has been added.

Claim 52 serves as a base claim for claims 53-57. Claims 58-63 recite a method of use. Support for these amendments may be found throughout the Specification, and at least at the exemplary Paragraphs noted in the table below. Accordingly, as to these claims, no new matter has been added.

Claim	specification
52. (New) A vaccine comprising a nucleic acid having a nucleotide sequence with at least 90% sequence	The present invention relates to vaccines comprising a nucleotide sequence ... selected from SEQ ID No. 15 (para. 15). Homologous nucleotide sequence in the sense of the present invention is understood as meaning a nucleotide

identity to SEQ ID No. 15 and an acceptable pharmaceutical vehicle,	sequence having at least a percentage identity with the bases of a nucleotide sequence according to the invention of ... preferably 90% or 95% (para. 57).
wherein said nucleic acid encodes an immunogenic protein that induces a protective response effective against infection by a piglet weight loss disease circovirus,	Examples 5-8.
wherein said vaccine does not comprise naturally occurring porcine circovirus.	It must be understood that the present invention does not relate to the genomic nucleotide sequences taken in their natural environment, that is to say in the natural state. (para. 53).

Rejections under § 102(e)

Claims 17 and 19-21 were rejected as anticipated under § 102(e) by the following two patents: U.S. Pat. No. 6,368,601 and U.S. Pat. No. 6,660,272. Office action, pp. 2-3.

Withdrawal of the rejection is respectfully requested.

Specifically, claim 17 reads as follows:

17. (Currently Amended) A vaccine comprising **[[a]] an isolated** nucleic acid having a nucleotide sequence with at least 90% sequence identity to SEQ ID No. 15 and an acceptable pharmaceutical vehicle, wherein said nucleic acid encodes an immunogenic protein that induces a protective response effective against infection by a piglet weight loss disease circovirus, **wherein said nucleotide sequence comprises a sequence having at least 90% sequence identity to at least one of SEQ ID No. 23 and SEQ ID No. 25.**

It is submitted that both the '601 and the '272 patents fail to describe such a vaccine for the reasons stated in the next subsections. Thus, the rejection is avoided and should be withdrawn.

The third subsection of this section will distinguish the new claims from the cited references.

An anticipation rejection under § 102(e) requires that a prior art patent *describe* the claimed invention.¹ As used in § 102, "described" has a particular meaning. A prior art reference describes a claim of an application only if each and every element as set forth in each claim is found, either expressly or inherently, in a single reference. M.P.E.P. § 2131. This description requires much more than finding each and every element in a prior art reference: "The identical invention must be shown in as complete detail as is contained in the ... claim." See M.P.E.P. § 2131 (quoting *Richardson v. Suzuki Motor Co.*, 868 F.2d 1226, 1236, 9 U.S.P.Q.2d 1913, 1920 (Fed. Cir. 1989)). **The reference must direct those skilled in the art to the presently claimed invention without any need for picking, choosing, and combining various disclosures in the reference not directly related to each other by the teachings of the cited reference.** See *In re Arkley*, 455 F.2d 586, 587, 172 USPQ 524, 526 (CCPA 1972).

Here, neither the '601 patent nor the '272 patent meet this standard.

The '601 patent.

According to the rejection, "Allan et al disclosed the ORFs 1-13 of circovirus type II (see claim 9). This is supposed to be the entire virus, where it can be reasonably inferred comprises the ORF2 and thus the composition of claim 17." Office action at 2.

However, claim 9 fails to direct those skilled in the art to a particular vaccine, let alone a particular ORF, let further alone a particular porcine circovirus. Claim 9 reads as follows:

9. A vector comprising an isolated DNA molecule comprising a sequence selected from the group consisting of 30 ORFs 1 to 13 of porcine circovirus type II.

¹ "A person shall be entitled to a patent unless ... (e) the invention was described in - ... (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent" 35 U.S.C. § 102.

Present claim 17 recites a “*vaccine ...wherein said nucleic acid encodes an immunogenic protein that induces a protective response effective against infection by a piglet weight loss disease circovirus.*” Claim 9 from the ‘601 patent, on the other hand, fails to describe, let alone enable one to make, any particular *vaccine*.

Furthermore, the ‘601 patent is, at best, an invitation to find the actual ORFs and to experiment to find a structural protein, which is clearly stated in the following paragraph:

55 It appears that the genomic organization of the porcine circovirus is quite complex as a consequence of the extreme compactness of its genome. The major structural protein is probably derived from splicing between several reading frames situated on the same strand of the porcine circovirus genome. It can therefore be considered that any open reading
60 frame (ORF1 to ORF13) as described in the table above can represent all or part of an antigenic protein encoded by the type II porcine circovirus and is therefore potentially an antigen which can be used for specific diagnosis and/or for vaccination. The invention therefore relates to any protein
65 comprising at least one of these ORFs. Preferably, the invention relates to a protein essentially consisting of ORF4, ORF7, ORF10 or ORF13.

The ‘601 patent, col. 14, ll. 53-66. Indeed, such a description—e.g., any open reading frame ... can represent all or part of an antigenic protein encoded by [PCV] II ... and ... is potentially an antigen—merely represents a “wish to know the identity” of the ORF or ORFs encoding a structural protein and cannot be equated with a description that immunoprotection is correlated to a particular, stated structure, namely, the full length strain and its putative ORFs. For sure, this description represents merely a “wish” or “plan,” the words of *Fiers v. Revel*, 984 F.2d 1164, 1171 (Fed. Cir. 1993); *see also Amgen Inc. v. Hoechst Marion Roussel, Inc.*, 314 F.3d 1313, 1332 (Fed. Cir. 2003). It cannot direct those skilled in the art to any particular ORF.

Compounding the lack of description for the ORF is the fact that claim 9 does not refer to any particular porcine circovirus but to a family of porcine circoviruses. The ‘601 patent fails to disclose the partial structure common to all known circoviruses. It fails to disclose functional

characteristics that distinguish it from other porcine circoviruses and a correlation between that function and structure. Clearly, the '601 patent fails to describe all porcine circoviruses, and more importantly, fails to direct those skilled in the art to any vaccine, let alone one comprising a particular porcine circovirus or a particular ORF.

Along these lines, the '601 patent prophetically describes a generic *vaccine*—but never describes particular circoviruses (or OFRs) useful for the prophetic vaccine—in the following passages containing Examples 17-18:

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The aqueous phase and the oily phase are sterilized separately by filtration. The emulsion is prepared by mixing and homogenizing the ingredients with the aid of a Silverson turbine emulsifier.

One vaccine dose contains about $10^{7.5}$ TCID₅₀. The volume of one vaccine dose is 0.5 ml for administration by the intradermal route, and 2 ml for administration by the intramuscular route.

Example 18

Preparation of the vaccine in the form of a metabolizable oil-based emulsion.

The vaccine is prepared according to the following formula:

suspension of inactivated porcine circovirus: 200 ml

Dchymuls HRE 7 (Henkel): 60 ml

45 Radia 7204 (Oleofina): 740 ml

The aqueous phase and the oily phase are sterilized separately by filtration. The emulsion is prepared by mixing and homogenizing the ingredients with the aid of a Silverson turbine emulsifier.

One vaccine dose contains about $10^{7.5}$ TCID₅₀. The volume of one vaccine dose is 2 ml for administration by the intramuscular route.

Example 17

Preparation of the vaccine in the form of an emulsion based on mineral oil.

The vaccine is prepared according to the following formula:

suspension of inactivated porcine circovirus: 250 ml

Montanide® ISA 70 (SEPPIC): 750 ml

What is the “inactivated porcine circovirus” mentioned at column 15, line 48 or column 16, line 43? These examples never describe any inactivated PCV, let alone an inactivated PCV II, or *an isolated nucleic acid* thereof. The above generic description, however, is not enabling as to making a vaccine that would reasonably be expected to have activity *in vivo*. The examples fail to direct those skilled in the art to any particular vaccine.

In conclusion, none of the cited passages provides an enabling disclosure of all the elements of any rejected claim. Accordingly, the rejection should be withdrawn.

The '272 patent.

According to the rejection, “Claims 1, 2, 12, 18 of ‘272 are directed to the entire circovirus type II which reads on the broad claim 17.” Office action at 3. Applicants respectfully traverse this rejection.

Claims 1, 2, 12-13, and 18 of the ‘272 patent are not supported by the original filed disclosure. Claims 1, 2, 12-13 and 18 read as follows:

1. An isolated porcine circovirus type II.
2. The isolated porcine circovirus type II of claim 1 deposited at the ECACC and selected from the group consisting of: porcine circovirus type II accession No. V97100219, porcine circovirus type II accession No. V97100218, porcine circovirus type II accession No. V97100217, porcine circovirus type II accession No. V98011608, and porcine circovirus type II accession No. V98011609.
12. An immunogenic composition comprising an isolated porcine circovirus type II.
13. The immunogenic composition of claim 12 wherein the porcine circovirus type II is an attenuated porcine circovirus type II.
18. The immunogenic composition of claim 13, further comprising an adjuvant.

The originally filed disclosure does not teach the particular combination of elements recited in the claims. A generic original disclosure embracing many different possible combinations of elements cannot be used to anticipate a single specific group of elements or small group of species. The claims of the ‘272 patent cited in the rejection were not in the as-filed application that produced the ‘272 patent. On June 19, 2001, well after the present application’s immediate parent (the ‘245 application’s) application’s filing date of February 28, 2000, Allen et al. canceled all as-filed claims and replaced them with claims 42-57. As a result, no claim from Allan et al. is evidence that the ‘272 patent described the presently claimed invention before the effective date of the presently rejected claims.

Moreover, the ‘272 patent prophetically describes a *vaccine* in the following passages containing Examples 17-18.

16

suspension of inactivated porcine circovirus:	250 ml
Montanide ® ISA 70 (SEPPIC):	750 ml

The aqueous phase and the oily phase are sterilized separately by filtration. The emulsion is prepared by mixing and homogenizing the ingredients with the aid of a Silverson turbine emulsifier.

One vaccine dose contains about $10^{7.5}$ TCID₅₀. The volume of one vaccine dose is 0.5 ml for administration by the intradermal route, and 2 ml for administration by the intramuscular route.

Example 18

Preparation of the Vaccine in the Form of a
Metabolizable Oil-Based Emulsion

The vaccine is prepared according to the following formula:

suspension of inactivated porcine circovirus:	200 ml
Dehymuls HRE 7 (Henkel):	60 ml
Radia 7204 (Oleofina):	740 ml

Example 17

Preparation of the Vaccine in the Form of an
Emulsion Based on Mineral Oil

The vaccine is prepared according to the following formula:

The aqueous phase and the oily phase are sterilized separately by filtration. The emulsion is prepared by mixing and homogenizing the ingredients with the aid of a Silverson turbine emulsifier.

These examples are just like those from the '601 patent (quoted above) in at least one respect, namely, neither example states the type of porcine circovirus. So, in Examples 17-18 it is unknown if the vaccine of type I or II or other, because each passage merely reads: "suspension of inactivated porcine circovirus...." Therefore, because there is uncertainty, there can be no inherent disclosure of *vaccine* as recited in the rejected claims. The examples fail to direct those skilled in the art to any particular vaccine.

In conclusion, none of the cited passages provides an enabling description of all the elements of any rejected claim. Accordingly, the rejection should be withdrawn.

New Claims

The new claims avoid the cited reference. Specifically, claims 29 and 41 respectively read as follows:

wherein said nucleotide sequence comprises a sequence having at least 90% sequence identity to at least one of SEQ ID No. 23 and SEQ ID No. 25; and

wherein said nucleotide sequence comprises a sequence having at least 95% sequence identity to at least one of SEQ ID No. 23 and SEQ ID No. 25.

Similarly, claim 29 serves as the base claim for claims 30-40, claims 75-86 recite a method of use. Claim 41 serves as a base for claims 42-51, and claims 64-74 recite a method of use. For analogous reasons to claims 29 and 41, these claims are patentable.

Also, claim 52 reads as follows: wherein said vaccine does not comprise naturally occurring porcine circovirus. Claim 52 serves as a base claim for claims 53-57. Claims 58-63 recite a method of use. For analogous reasons to claim 52, these claims are patentable.

Rejection Under § 112, ¶ 2

Claims 17, 20, 23, and 26 were rejected as indefinite for reciting the terms "90% identity" or "95% identity." Office action, pp. 3-4. According to the rejection, "there are no indications of the utilized algorithm to calculate the identity sequences." Office action, p. 4. The rejection is respectfully traversed.

The present specification provides clear and ample disclosures of how to determine "percentage of sequence identity" (see paragraphs 0061-64). According to the specification, "percentage of sequence identity" is determined by comparing two "optimally aligned" sequences over a comparison window. Then, the specification describes algorithms that can be used for the optimal alignment. Furthermore, the specification explains how to calculate the percentage of identity, which does not need to use any algorithms. With the disclosure of algorithms combined with the sufficient descriptions of how to obtain percentage of sequence identity, one of ordinary

skill in the art would easily understand the scope of the rejected claims with a reasonable degree of particularity and certainty. Therefore, Applicants respectfully request reconsideration and withdrawal of the rejection.

Objection to the Claims

Claim 28 was rejected as not further limiting a prior base claim. Office action, p. 4.
Claims 23 and 26-28 read, with emphasis added, as follows:

23. (Currently Amended) A method of immunizing a mammal against piglet weight loss disease comprising administering to a mammal an effective amount of a vaccine, wherein said vaccine comprises **[[a]] an isolated** nucleic acid having a nucleotide sequence with at least ***90% sequence identity to SEQ ID No. 15*** and an acceptable pharmaceutical vehicle, wherein said nucleic acid encodes an immunogenic protein that induces a protective response effective against infection by a piglet weight loss disease circovirus, **wherein said nucleotide sequence comprises a sequence having at least 90% sequence identity to at least one of SEQ ID No. 23 and SEQ ID No. 25.**

26. (Previously Presented) A method according to claim 23, wherein said nucleic acid has a nucleotide sequence with at least ***95% sequence identity to SEQ ID No. 15.***

27. (Previously Presented) A method according to claim 26, wherein said vaccine ***further comprises an adjuvant.***

28. (Previously Presented) A method according to claim 27, wherein said nucleotide sequence ***is SEQ ID No. 15.***

As can be clearly seen in the highlighted-italicized text, the scope of claim 28 is narrowed (by reciting “***is SEQ ID No. 15***”) compared to claims 27, 26, or 23. Thus, the objection should be withdrawn.

Rejection Under § 112, ¶ 1 (enablement)

Claims 17-28 were rejected as non-enabled by the specification, because “[t]he current specification does not teach nor [enable] a vaccine to induce a protective response wherein upon introduction of the specific antigens or fragments thereof [into] a host a protective response can be inferred.” Office action, p. 5. The present rejection is respectfully traversed.

Claims 17-28 recite “SEQ ID No 15,” which contains ORF’2 and ORF’1. These ORF’s, according to Example 8 of the present specification, were capable of producing protection: “Expression of PCV-B ORF’2 or PCV-B ORF’1 in swine resulted in a significantly enhanced level of protection as evaluated by weight evolution and body temperature evolution following challenge with PCV-B circovirus.” (Generally, paragraphs 341-50, pages 77-79; specifically, paragraph 349, page 79). Thus, it is submitted that a protective response can be inferred from these examples.

The rejection improperly ignored the functional language in the claims under examination. For example, claim 17 recites *vaccine ...wherein said nucleic acid encodes an immunogenic protein that induces a protective response effective against infection by a piglet weight loss disease circovirus*. One of ordinary skill in the art, guided by the present specification, could find such a *nucleic acid with no more than routine experimentation*.

For example, SEQ ID NO. 15 contains PCV-B ORF’2 (SEQ ID No 25) or PCV-B ORF’1 (SEQ ID No 23). These ORFs were expressed. They resulted in a significantly enhanced level of protection. They allow one of ordinary skill in the art to infer a protective response. Clearly, one of ordinary skill in the art, guided by the present specification, should have been able to find such a *nucleic acid* for use in the *vaccine* as recited.

Also, from these data (protective response, ORFs, etc.), it is submitted that one of ordinary skill in the art, guided by the present specification, would have been able to decide what residues were candidates to be changed; which substitutions, deletions, or insertions may be made, and where those changes may be made. Indeed, the codon-amino acid residue relationship is known, the non-expressed regions of SEQ ID NO: 15 may be determined, and conservative

amino acid substitutions are readily obtainable. Then, using the procedures of the present specification, one of ordinary skill in the art would have been able to find such a *nucleic acid* as recited and thus make and use a *vaccine* as recited.

Rejection Under § 112, ¶ 1 (written description)

Claims 17, 19-21, 23, and 25-28 were rejected as lacking a written description, because “[n]o other sequences [besides SEQ ID NO: 15] having percent identity of 90% or 95% were disclosed.” Office action, 6. The present rejection is respectfully traversed.

The structure of SEQ ID NO: 15 is stated. This structure contains two ORFs (SEQ ID NOS: 23 & 25) that were actually reduced to practice. These actual examples disclose a correlation between structure and function of SEQ ID NO: 15.

This structure-function relationship allows one of ordinary skill in the art to draw inferences. It is submitted that one of ordinary skill in the art, guided by the present specification, would have been able to decide what residues were candidates to be changed; which substitutions, deletions, or insertions may be made, and where those changes may be made. Indeed, the codon-amino acid residue relationship is known, the non-expressed regions of SEQ ID NO: 15 may be determined, and conservative amino acid substitutions are readily obtainable. Then, using the procedures of the present specification, one of ordinary skill in the art would have been able to find such a *nucleic acid* as recited and thus make and use a *vaccine* as recited.

Other Applications

Earlier filed IDSs identified for the Examiner’s convenience the related family members. Subsequent to the filing of the last IDS, Applicants wish to update the Examiner about the filing of an additional family member. New application 11/317,260 was filed on December 23, 2005, which application is a continuation of 11/007,798, filed December 9, 2004, which is a continuation of 10/682,420, filed October 10, 2003, which is a continuation of 10/637,011, filed August 8, 2003, which is a Continuation of 09/514,245 filed February 28, 2000, now U.S. Patent

No. 6,703,023, which application is a continuation-in-part of PCT/FR98/02634, filed December 4, 1998.

Also, new U.S. application no. 11/262,514 was filed on October 31, 2005, which application is pending and claims the benefit of U.S. Application no. 10/775,337, filed February 11, 2004 (abandoned), which is a continuation of U.S. Application no. 09/514,245, filed February 28, 2000, now Patent No. 6,703,023, which is a continuation-in-part of International Application no. PCT/FR98/02634, filed December 04, 1998.

Furthermore, on July 8, 2005, Applicants filed another application no. 11/176,667. which is a continuation of U.S. Application no. 09/514,245, filed February 28, 2000, now Patent No. 6,703,023, which is a continuation-in-part of International Application no. PCT/FR98/02634, filed December 04, 1998.

The mention of any application herein, including but not limited to the '798 application, is not a waiver of the application's secrecy.

The Examiner is thanked for citing the publication no. 2002-0106639 A1 ("Wang '639"). Along these lines, the Examiner's attention is directed to application nos. 10/637,011, filed August 8, 2003, and 11/176,667, filed July 8, 2005.

The mention of any application herein, including but not limited to the '798 application, is not a waiver of the application's secrecy.

An IDS accompanies this paper.

Wang '639 and a Comparison

It is submitted that (a) Wang '639 does not teach, possess or enable a DNA vaccine for circovirus as claimed and that (b) Wang '639 provides a large genus of potential sequences that, at best, might be used to try to discover such a vaccine, but no guideposts pointing towards any particular vaccine, let alone one at least 90% of ORF2 or ORF1 as a component to achieve immunoprotection in live animals. Comments about Wang '639 precede a comparison.

I. Wang '639

Wang '639, titled *Postweaning multisystemic wasting syndrome virus from pigs*, names four Inventors (Wang, Li; Babiuk, Lorne A.; Potter, Andrew A.; and Willson, Philip), and is assigned on its face to the University of Saskatchewan. It resulted from application no. 09/935,428, filed August 20, 2001.

The '428 application claims priority to application no. 09/209,961, filed December 10, 1998 (Wang '639's parent application), which application claimed the benefit of provisional application nos. 60/069,233, filed December 11, 1997 (Wang's provisional I), and 60/069,750, filed December 16, 1997 (Wang's provisional II).

Wang '639 claims to describe three isolated DNAs from type II porcine circovirus (PCVII) labeled SEQ ID NOS:1, 11, and 12. Wang '639 also claims to describe multiple ORFs 6 [think of them as 6 long and 6 short, *vide infra*] of SEQ ID NO: 1, which will be discussed before commenting on SEQ ID NO: 12, on SEQ ID NO: 1& 11, and then on all the isolates in general.

Figure 2A-C shows SEQ ID NO: 1, as well as the proteins encoded by putative (computer found) ORF 1-6 sequences contained within SEQ ID NO: 1. Some of the encoded proteins are said to be shown in Figures 3A-C. According to Wang '639, some of the encoded proteins are in the sequence listing as follows: ORF 1 (SEQ ID NO: 3), ORF 2 (SEQ ID NO: 9), ... and ORF 6 (SEQ ID NO: 5).

Upon close examination, however, Wang '639 refers to the amino acid encoded by ORF 6 in inconsistent ways. On one hand, as just mentioned, the amino acid encoded by ORF 6 is said to be SEQ ID NO: 5, a 233 amino acid polypeptide. On the other hand, Wang identifies the encoded polypeptide as the amino acids on the top line of Figure 3B, a ~261 amino acid polypeptide, which differs from SEQ ID NO: 5 at least by having an extra 28 or so amino acid residues (see the beginning of Figure 3B, reading MLL ... FSA).

It is submitted that Wang '639 does not describe a nucleic acid encoding the ~261 amino acid polypeptide of Figure 3B. In other words, Wang '639 lacks a written description for a nucleic acid encoding the ~261 amino acid polypeptide of Figure 3B, let alone a vaccine comprising such a nucleic acid. Thus, as to a vaccine comprising a nucleic acid encoding the ~261 amino acid polypeptide of Figure 3B, Wang '639 is not entitled to its actual U.S. filing date (August 20, 2001) or any of its effective U.S. filing dates (December 10, 1998, December 16, 1997, or December 11, 1997).

Similarly, upon close examination, Wang '639 describes all three isolates in inconsistent ways. On one hand, for example, Wang '639's SEQ ID NO: 12 is described as 240 base pairs in the sequence listing. SEQ ID NO: 12's length (240 bp) is much shorter than the length SEQ ID NOs:1 & 11 (1768 bp), which strongly suggests that SEQ ID NO: 12 is not a complete sequence for the isolate. On the other hand, in Figure 4A, under B9 (which was equated to SEQ ID NO: 12 in paragraph 0010), the term "missing" appears at least twice. See rows 3-4, left side. Clearly, the skilled artisan would not be able to make B9 from Wang '639's disclosure. On top of this missing information, the required deposit information is missing from paragraph 199. *Cf.* Rule 809(d). Clearly, the skilled artisan would not be able to make B9 from Wang '639's disclosure, nor would the skilled artisan equate the 240 bp SEQ ID NO: 12 with the other PCVII isolates.

As a result, Wang '639 lacks a written description for a nucleic acid of the isolate SEQ ID NO: 12 and/or B9, let alone a vaccine comprising either nucleic acid. Thus, as to a vaccine comprising Wang '639's SEQ ID NO: 12 and/or B9, Wang '639 is not entitled to its actual U.S. filing date (August 20, 2001), let alone any of its effective U.S. filing dates (December 10, 1998, December 16, 1997, or December 11, 1997). Wang '639 clearly did not possess this subject matter at the time of any of its several filing dates.

Similarly, Wang '639 describes the other two isolates (412 & 9741) in inconsistent ways. In SEQ ID NOs 1 & 11, the nucleotide at position 401 is a T (see attachment, circling the

nucleotide with a “star”). In Figure 4A of Wang ‘639, the same nucleotide is a C. For sure, Wang ‘639 did not consistently describe what was possessed. See, also, attachments from Wang’s provisionals I & II, with markings on the relevant nucleotide.

Regarding each isolate, Wang ‘639 discloses a wish to make protein based vaccine formulations (see, e.g., paragraphs 113-125) and makes reference in a very cursory way to the possibility of using DNA directly for a vaccine (see, e.g., paragraph 126) or gene therapy (see, e.g., paragraph 127). For example paragraph 126 reads as follows:

[0126] The proteins of the instant invention can also be administered via a carrier virus which expresses the same. Carrier viruses which will find use with the instant invention include but are not limited to the vaccinia and other pox viruses, adenovirus, and herpes virus. By way of example, vaccinia virus recombinants expressing the novel proteins can be constructed as follows. The DNA encoding the particular protein is first inserted into an appropriate vector so that it is adjacent to a vaccinia promoter and flanking vaccinia DNA sequences, such as the sequence encoding thymidine kinase (TK). This vector is then used to transfect cells which are simultaneously infected with vaccinia. Homologous recombination serves to insert the vaccinia promoter plus the gene encoding the instant protein into the viral genome. The resulting “TK” recombinant can be selected by culturing the cells in the presence of 5-bromodeoxyuridine and picking viral plaques resistant thereto.

Wang ‘639, ¶126. Wang ‘639, however, describes no working examples preparing or using a vaccine, and Wang ‘639 contains no detailed discussion of how a DNA vaccine would be prepared or used. At best, all Wang ‘639 described were the sequences of two isolates and putative ORFs most likely chosen by an algorithm. It is submitted that such wishes or plans are, at best, an invitation for future research rather than sufficient written description enabling one to make a vaccine.

Along these lines, the present Examiner has considered Wang ‘639 and Wang’s provisionals I & II, but did not make a rejection of the present claims as anticipated by Wang ‘639 under §102(e)(1) or obvious over Wang ‘639 under §103(a). The present Examiner also found Wang ‘639’s written description to be non-enabling as to DNA vaccines during the prosecution of Wang ‘639’s parent application. These facts are consistent with Wang ‘639 being non-enabling as to DNA vaccines. Office action in Wang ‘961, paper 8, p. 4 (enclosed for

consideration). Thus, as to a vaccine comprising a nucleic acid, Wang '639 is not entitled to its actual U.S. filing date (August 20, 2001), or its effective U.S. filing date (December 10, 1998) and/or the filing date of Wang's provisionals I and/or II (December 1997).

II. Comparison

For the Examiner's consideration, the undersigned includes a preliminary comparison of DNA and amino acid sequences of the present application with analogous sequences of Wang '639.

A. Wang's Sequences (not necessarily Wang '639's sequences)

As noted above, at least some of Wang '639's sequences were inconsistently described. So, for ease of comparison, Wang's sequences were taken from GENBANK, and the GENBANK sequences were at least partially eye-checked (proofread) to see if they correspond to what was actually described in Wang '639 or Wang's provisionals I & II.

GenBank #	Cf. SEQ ID
AF085695	SEQ ID No: 1
AF086835	SEQ ID No: 11
AF086834	SEQ ID No: 12

The following remarks report the undersigned's observations.

SEQ ID NO: 1 in Wang '639 and AF085695 are the same. SEQ ID NO: 1 in Wang '639 and the data from figure 6 in Wang's provisional II differ in at least one nucleotide (see the "star" in SEQ ID NO: 1 of the attachment and Fig. 6A of the attachment). Such minor differences, however, will not have a large effect on an analysis of percentage homology of a 1768 bp sequence comparison, e.g., Jestin's SEQ ID NO: 15 v. Wang's 412 (Figure 6A or SEQ ID NO: 1).² Thus, with these differences of Wang's 412 isolate in mind, AF085695 was compared against Jestin's SEQ ID NO: 15 (*vide infra*).

² Even if the data from Figure 4 in the Wang '639 publication and the data from figure 6 in Wang's provisional II appear to be identical, the undersigned has yet to proofread these figures.

SEQ ID NO: 11 in Wang '639 and AF086835 differ by at least three nucleotides (see SEQ ID NO: 11 of the attachment). Similarly, SEQ ID NO: 11 in Wang '639 and the data from figure 6 in Wang's provisional II differ in at least one nucleotide (see SEQ ID NO: 11 of the attachment and figure 6A of the attachment). Such difference, however, will not have a large effect on the percentage homology of a 1768 nucleotide sequence comparison, e.g., Jestin's SEQ ID NO: 15 v. Wang's 9741 (Figure 6A or SEQ ID NO: 11 or AF086835). Thus, with these differences of Wang's 9741 isolate in mind, AF086835 was compared against Jestin's SEQ ID NO: 15 (*vide infra*).³

As noted above, Wang '639 lacks a written description for a nucleic acid of the isolate SEQ ID NO: 12 and/or B9. Thus, AF086834 does not correspond to anything in Wang '639, but AF086834 was checked anyway.

BLASTn analysis results were generated and are reported below. BLAST was found at <http://www.ncbi.nlm.nih.gov/BLAST/>.⁴

B. The Sequences of the present Application

The present application describes full-length DNA (SEQ ID NO: 15 and SEQ ID NO: 19) and three of its fragments SEQ ID NOs: 23, 25, and 27, which fragments correspond to ORFs '1, '2, and '3, respectively.

C. DNA Comparison

The present application's full-length SEQ ID NO: 15 is comparable to Wang's full-length circovirus sequences, namely, SEQ ID NO: 1, SEQ ID NO: 11 and SEQ ID NO: 12 from

³ Even if the data from Figure 4 in Wang '639 and the data from figure 6 in Wang's provisional II appear to be identical, these data were not proofread, and the same comments regarding Wang's 412 isolate apply for Wang's 9741, too.

⁴ The pinpoint changes were not checked to see if they affect the ORFs and, if they do, the translated amino acids. The Examiner is invited to contact the undersigned if he wants such information to be generated.

GENBANK. Jestin's SEQ ID NO: 15 is 94-95% identical to each of the three full-length circovirus sequences from LGENBANK. *See* Table 1.

Table 1: Comparison of Full-Length DNA Sequences (% Identity)

JESTIN	WANG (GENBANK) SEQ ID NO: 1	WANG (GENBANK) SEQ ID NO: 11	WANG (GENBANK) SEQ ID NO: 12
SEQ ID NO: 15	95%	95%	94%

(No inference should be drawn by the use of two significant figures. Rounding was used. Actual numbers will be made available upon request. *See* attached raw data) Note that Wang '639's SEQ. ID. NO: 12, as disclosed in Wang '639, is 240 nucleotides and could not be aligned to the same extent as AF086834, i.e., 94%, because SEQ ID NO: 12 is too short.

The present application's ORFs SEQ ID NO: 23, SEQ ID NO: 25 and SEQ ID NO: 27 have some partial similarity with each of Wang's full-length circoviruses. For example, SEQ ID NO: 25 is 93% identical to the analogous sequences within each circovirus from GENBANK. *See* Table 2.

Table 2: Comparison of Fragment DNA Sequences (% Identity)

JESTIN	WANG (GENBANK) SEQ ID NO: 1	WANG (GENBANK) SEQ ID NO: 11	WANG (GENBANK) SEQ ID NO: 12	WANG's Putative ORF Alignment*
SEQ ID NO: 23	96%	95%	95%	ORF 1
SEQ ID NO: 25	93%	93%	93%	ORF 6
SEQ ID NO: 27	96%	96%	96%	ORF 2

*In Table 2, "ORF alignment" refers to the analogous putative ORFs of Wang '639. It is not an admission that Wang '639 consistently describes any ORF in the family of applications related to Wang '639. For example, ORF 6 is comparable to SEQ ID NO: 25 of the present application.

D. Peptide Comparison

The peptides encoded by Jestin's SEQ ID NO: 23, SEQ ID NO: 25 and SEQ ID NO: 27 were compared to analogous peptides encoded by putative ORFs of Wang (GENBANK) as determined, *e.g.*, by Examiner Pasy (us.ExPasy.org/tools/dng.html). *See* Table 3.

Table 3: Comparison of Peptide Sequences

Peptide Sequence Encoded By JESTIN's ORFs	Peptide Sequence Encoded By Wang Putative ORF	Amino Acid Comparison (Identical Amino Acids/Total Amino Acids)	% Identity Based On Amino Acid Comparison
SEQ ID NO: 23	ORF 1	303/314	96%
SEQ ID NO: 25	ORF 6	217/233	93%
SEQ ID NO: 27	ORF 2	95/104	91%

For example, the peptide encoded by Jestin's SEQ ID NO: 25 is 93% identical to that encoded by putative ORF 6. In other words, 217 of 233 amino acids encoded by Jestin's SEQ ID NO: 25 are the same as those encoded by putative ORF 6.

The foregoing analysis is provided for the Examiner's convenience in assessing Applicants' new and amended claims. However, Applicants submit that regardless of any level of sequence similarity between the sequences of Wang '639 and Applicants' sequences, Wang '639 does not teach, possess or enable one to make or use a DNA vaccine for circovirus as presently claimed.

General

The Examiner is thanked for granting the interviews in this matter. It is believed that the substance of the interview may be learned from these remarks.

Conclusion

Reconsideration and reexamination of the present application is respectfully requested.
Please contact the undersigned if any matters may be resolved by a telephone conference.

Respectfully submitted,

Date 01-12-2006

FOLEY & LARDNER LLP

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By

 (45943)

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Registration No. 35,264

Should additional fees be necessary in connection with the filing of this paper, or if a petition for extension of time is required for timely acceptance of same, the Commissioner is hereby authorized to charge Deposit Account No. 19-0741 for any such fees; and applicant(s) hereby petition for any needed extension of time.

ENCLOSURES: Office action in Wang '961, paper 8; US2002-0106639, pp. 18 & 25 with interlineations; Figure 6A from 60/069,750 with interlineations; Figure 4A from 60/069,233, with interlineations; and 32 pages of raw BLASTn Results, with interlineations for determining BLASTn parameters.



**UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office**

Address: COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
09/209,981	12/10/98	WANG	9000-0040

ROBINS & ASSOCIATES
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HM22/0121

EXAMINER
SALIMI, A

ART UNIT	PAPER NUMBER
1645	8

DATE MAILED: 01/21/00

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks



Office Action Summary	Application No. 09/209,961	Applicant(s) Wang et al
	Examiner ALI R. SALIMI	Group Art Unit 1645

☒ Responsive to communication(s) filed on Nov 15, 1999

☐ This action is **FINAL**.

☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11; 453 O.G. 213.

A shortened statutory period for response to this action is set to expire Three month(s), or thirty days, whichever is longer, from the mailing date of this communication. Failure to respond within the period for response will cause the application to become abandoned. (35 U.S.C. § 133). Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

Disposition of Claims

☒ Claim(s) 1-47 is/are pending in the application.

Of the above, claim(s) 1-6, 10, 11, 15, 16, 20, 21, and 25-47 is/are withdrawn from consideration.

☐ Claim(s) _____ is/are allowed.

☒ Claim(s) 7-9, 12-14, 17-19, and 22-24 is/are rejected.

☐ Claim(s) _____ is/are objected to.

☐ Claims _____ are subject to restriction or election requirement.

Application Papers

☐ See the attached Notice of Draftsperson's Patent Drawing Review, PTO-948.

☐ The drawing(s) filed on _____ is/are objected to by the Examiner.

☐ The proposed drawing correction, filed on _____ is ☐ approved ☐ disapproved.

☐ The specification is objected to by the Examiner.

☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. § 119

☐ Acknowledgement is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d).

☐ All ☐ Some* ☐ None of the CERTIFIED copies of the priority documents have been

☐ received.

☐ received in Application No. (Series Code/Serial Number) _____

☐ received in this national stage application from the International Bureau (PCT Rule 17.2(a)).

*Certified copies not received: _____

☒ Acknowledgement is made of a claim for domestic priority under 35 U.S.C. § 119(e).

Attachment(s)

☒ Notice of References Cited, PTO-892

☒ Information Disclosure Statement(s), PTO-1449, Paper No(s). 4, 5

☐ Interview Summary, PTO-413

☐ Notice of Draftsperson's Patent Drawing Review, PTO-948

☐ Notice of Informal Patent Application, PTO-152

--- SEE OFFICE ACTION ON THE FOLLOWING PAGES ---

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Art Unit: 1645

DETAILED ACTION

The Group and/or Art Unit location of your application in the PTO has changed. To aid in correlating any papers for this application, all further correspondence regarding this application should be directed to Group Art Unit 1645.

Claims 1-47 are pending.

Raw Sequence Listing have been entered.

Submitted Information Disclosure Statement (I.D.S) is noted.

Election/Restriction

Applicant's election with traverse of Group II (claims 7-9, 12-14, 17-19, 22-24) in Paper No. 7 is acknowledged. The traversal is on the ground(s) that Applicants believe the examination of all groups is not unduly burdensome. This is not found persuasive because considering the separate classification and divergent search requirements of the distinct groups, it is maintained that examination of all groups would be unduly burdensome. Clearly different searches and issues are involved in the examination of each group, especially with respect of the percent identity limitations, derived fragments and immunogenic constructs, various sequence searches and different gap and default calculations need to be considered, both in the in house and commercial data bases.

The requirement is still deemed proper and is therefore made FINAL.

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Claims 1-6, 10, 11, 15, 16, 20, 21, 25-47 are withdrawn from further consideration by the examiner, 37 CFR 1.142(b), as being drawn to a non-elected groups, the requirement having been traversed in Paper No. 7.

Applicant is reminded to cancel the claims to the non elected claims.

Specification

The disclosure is objected to because of the following: The date and the designated accession number for the deposited virus are missing from the specification page 8, lines 29, and 30. Appropriate correction is required.

Claim Rejections - 35 USC § 112

Claims 7-9, 12-14, 17-19, 22-24 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 7-9 are vague and indefinite, the claims are very confusing. The metes and bounds of the derived polypeptide(s) is/are not defined. The intended derived polypeptide should be identified. Is a nucleic acid encoding five amino acid long and polypeptide having 85% identity of the said five amino acids intended? For example, SEQ ID NO: 3 is 314 amino acids long which translates into 942 nucleotides, what are the metes and bounds of polypeptides that are derived

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from SEQ ID NO: 3. In addition, the term "at least about" is unclear. Is about intended? Moreover, the metes and bounds of the intended fragments are not defined. This affects the dependent claims.

Claims 17-19 are confusing, does this read on gene therapy or DNA vaccines? Is induction of immune response intended? The claims have been interpreted in light of the specification, and since the specification does not have clear teaching as to what is intended the claims are hereafter objected to. Is the transformation, *in vivo*, or *in vitro*? This affects the dependent claims.

Claim Rejections - 35 USC § 112

Claims 7-9, 12-14, 17-19, 22-24 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for induction of antibody response, does not reasonably provide enablement for transformation of cells in inducing a protective response (vaccine). The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make or use the invention commensurate in scope with these claims. The scope of the claims read on transformation of the host cell which reads on a vaccine development. Applicants are reminded that the field of vaccine development is considered to be highly unpredictable. According to the specification and the state of the art the currently claimed virus attacks the immune system and disables the immune response. A vaccine

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is considered to be protective wherein upon re- introduction of the disease to induce a long lasting protective response against a challenge. The current specification does not teach nor enables a vaccine to induce a protective response wherein upon introduction of the specific antigens or fragments thereof in to a host a protective response can be inferred. Absent teaching by the specification it would require undue experimentation for one ordinary skill in the art to enable the scope of the claims. The specification provides no teaching as to the transformation and induction of immunogenic protective response against the claimed antigenic fragments. Therefore, considering large quantity of experimentation needed, the unpredictability of the field, the state of the art, and breadth of the claims, it is concluded that undue experimentation would be required to enable the invention.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless --

(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person

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having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

Claims 7-9 are rejected under 35 U.S.C. 102(a) as anticipated by or, in the alternative, under 35 U.S.C. 103(a) as obvious over Meehan et al (J of Gen. Virology, 1997, vol. 78, pp. 221-227).

The polypeptide and the nucleotide sequence disclosed by the above cited article meets the limitations of the claimed invention. In addition it also meets the limitations of derived and fragments. The above cited art meets the limitations of 85% identity, and immunogenic fragments of 5 at least about five amino acids, of the claimed limitation. Alternatively, it would have been obvious to one ordinary skill in the art to derive polypeptides from the disclosed sequence and utilize the fragments to enhance immune response. The ordinary skilled artisan being familiar with the state of the art and the cited article would not have anticipated any unexpected results. The claims are deemed *prima facie* obvious absent unexpected results.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

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Claims 7-9, 12-14, 17-19, 22-24 are rejected under 35 U.S.C. 103(a) as being unpatentable over Meehan et al (J of Gen. Virology, 1997, vol. 78, pp. 221-227) and Vogel et al (Clinical Microbiology Review, 1995, Vol. 8, No. 3, pp. 406-410).

The claims are directed to polynucleotide encoding an immunogenic polypeptide of circovirus Type II (PCVII), in addition to nucleotides having 85% identity to the polypeptides derived from various ORFs. In addition, the claims are directed to recombinant vector expressing the various polypeptide fragments derived from the said ORFs wherein the expression construct is derived by a foreign promoter. Furthermore, the claims are directed to host cells transformed by an expression vector encoding PCVII nucleotide to induce an immune response.

Meehan et al disclosed the complete nucleotide sequence of porcine circovirus. They further disclosed the genomic organization of the PCV genome (see the abstract, and page 223, right paragraph). This differs since they did not teach a vector and expression of the nucleic acids.

Vogel et al disclosed the use of DNA vaccines wherein a nucleic acid sequences is encoded within a vector with a heterologous promoter present to ensure high level of expression (see page 406, column 2, paragraph 2, and Figure 1). This differs since they did not teach the circovirus genome.

Therefore, one of ordinary skill in the art at the time of filing would have been highly motivated by the above teaching to incorporate the nucleotide fragment sequences derived from the circovirus taught by Meehan et al into a vector taught by Vogel et al to transform the host cell

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in inducing an immunogenic response in a host. In addition, the utilization of vector in a method of producing polypeptide in cell culture is considered to be routine in this art. The skilled artisan being familiar with the genomic organization and nucleotide sequence of the said virus would not have anticipated any unexpected results. Thus, the invention as a whole is considered to be *prima facie* obvious absent unexpected results.

No claims are allowed.

Conclusion

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Ali Salimi whose telephone number is (703) 305-7136. The examiner can normally be reached on Monday-Friday from 9:00 Am to 6:00 Pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Anthony Caputa, can be reached on (703) 308-3995. The fax phone number for this Group is (703) 305-7401.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Ali R. Salimi

1/19/2000


ALI SALIMI
PATENT EXAMINER

assigned Accession No. . The accession number indicated was assigned after successful viability testing, and the requisite fees were paid. The deposits were made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of viable cultures for a period of thirty (30) years from the date of deposit. The organisms will be made available by the ATCC under the terms of the Budapest Treaty, which assures permanent and unrestricted availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 U.S.C. §122 and the Commissioner's rules pursuant thereto (including 37 C.F.R. §1.12 with particular reference to 886 OG 638). Upon the granting of a patent, all restrictions on the

availability to the public of the deposited cultures will be irrevocably removed.

[0200] These deposits are provided merely as convenience to those of skill in the art, and are not an admission that a deposit is required under 35 U.S.C. §112. The nucleic acid sequences of these genes, as well as the amino acid sequences of the molecules encoded thereby, are incorporated herein by reference and are controlling in the event of any conflict with the description herein.

[0201] Thus, the cloning, expression and characterization of novel PCVII isolates is disclosed, as are methods of using the same. Although preferred embodiments of the subject invention have been described in some detail, it is understood that obvious variations can be made without departing from the spirit and the scope of the invention as defined by the appended claims.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 24

<210> SEQ ID NO 1

<211> LENGTH: 1768

<212> TYPE: DNA

<213> ORGANISM: Porcine Circovirus Type II

<400> SEQUENCE: 1

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cttcgaaga cgagcgcaag aaaatacggg agctcccaat ctccctattt gattatttta 180
ttgttgccga ggagggtaat gaggaaggac gaacacctca cctccagggg ttgcctaatt 240
ttgtgaagaa gcaaaacttt aataaagtga agtggtattt ggggtgccgc tgccacatcg 300
agaaagccaa aggaactgat cagcagaata aagaattatg cagtaagaa ggcaacttac 360
ttattgaatg tggagctcct cgaatcgaag gacaacggag ttacctgtct actgctgtga 420
gtacottgtt ggagagcggg attctggtag ccgttgcaaa gcagcacctt gtaacgtttg 480
tcaaaaaatt ccgcgggctg gctgaacttt tgaagtgag cgggaaatg caaaagcgtg 540
attggaanaa caatgtacac ttcatgttgg ggccacctgg gtgtgtgaaa agcaaatggg 600
ctgctaattt tgcaaacccg gaaaccacat actggaacc acctaaaaa aagtgggtgg 660
atggttacca tgggtgaaaa gtggttgtaa ttgatgactt ttatggctgg ctgccgtggg 720
atgatctact gagaactgtg gatcgatato cattgactgt aaaaactaaa ggtggaaactg 780
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ggaagaatgc tacaanaaaa tccacggagg aagggggcca gttegtcacc ctttccccc 960
catgccctga atttccatat gaaataaatt actgagtctt ttttatcact tcgtaattgt 1020
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catacatggt tacacggata ttgtatgctt ggtcgtattt actgttttgg aacgcagtgc 1140
cgaggcctac gtggtccaca ttccagagg tttgtagcct cagccaaagc tgattccttt 1200
tgttatttgg ttggaagtaa tcaatagtgg agtcaagaac aggtttgggt gtgaagtaac 1260

SEE ALSO AF085695 FROM GENBANK.

☆ "C" in Figure 6A
OF Me 2d
Provisional '750
(60/069,750)

-continued

Leu Met Gly Leu Arg Ala Ala Phe Leu Ala Trp His Phe His
195 200 205

<210> SEQ ID NO 11
<211> LENGTH: 1768
<212> TYPE: DNA
<213> ORGANISM: Porcine Circovirus Type II
<400> SEQUENCE: 11

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cttcggaaga caagcgcaag aaaatacggg agctcccaat ctccctattt gattatttta 180
ttgttgcgga ggagggtaat gaggaaggac gaacacotca cctccagggg ttgctaat 240
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ctgtaattt tgcaaacccg gaaaccacat actggaaccc acctaaaaac aagtgtggg 660
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tacctttttt ggcccgcagt attctgatta ccagcaatca gaccocgttg gaatgtact 840
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tgttatttgg ttggaagtaa tcaatagtgg agtcaagaac aggtttgggt gtgaagtaac 1260
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catagggttag ggtgtggcc ttgttaaca agttatcacc taaaataaca gcagtggagc 1380
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ttattctgta gtattcaag ggtatagaga tttgttgggt ccccccctcc gggggaacaa 1500
agtcgtcaat tttaaatctc atcatgtcca cggccaggga gggcgttgg actgtggtac 1560
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tccaacggta gcggtggcg gggtggcga gccagggcg gcgagcggag atctggccaa 1680
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aaaacgaag aagtgcgtg taagtatt 1768

<210> SEQ ID NO 12
<211> LENGTH: 240
<212> TYPE: DNA

SEE ALSO AF086835
FROM GENBANK.

"C" IN FIGURE 6A
OF THE 2d PROVISIONAL
'750
(60/069,750)

TOO SHORT SEE ALSO AF086834 FROM
GENBANK, WHICH IS
1768 IN LENGTH.

0069780-1015

8915 ← INCOMPLETE.

FIG. 6A

WANG'S PROVISIONAL I

PHOS 412 1770 nt vs.
PCV 1759 nt
gap penalties: -12/-2; 76.0% identity; Global alignment score: 4035

```

      10      20      30      40      50      60
412  ACCAGCGCCTTCGGCAGCGGCAGCACCTCGGCAGCACCTCAGCAGCAACATGCCAGCA
      ::::: ::::: ::::: ::::: ::::: :::::
PCV  ACCAGCGCCTTCGGCAGCGGCAGCACCTCGGCAGCG--TCAGT--GAAATGCCAAGCA
      10      20      30      40      50

      70      80      90      100     110     120
412  AGAAGAATGGAAGAAGCGGACCCCAACCACATAAAAGGTGGGTGTTACGCTGAATAATC
      ::::: ::::: ::::: ::::: ::::: :::::
PCV  AGAA-----AAGCGGCCCGCAACCCCATAGAGGTGGGTGTTACCCCTTAATAATC
      60      70      80      90     100

      130     140     150     160     170     180
412  CTTCGGAAGACGAGCGCAAGAAAATACGGGAGCTCCCAATCTCCCTATTGATTATTTA
      ::::: ::::: ::::: ::::: ::::: :::::
PCV  CTTCGGAAGAGGAGAAAACAAAATACGGGAGCTTCCAATCTCCCTTTTGAATTATTTG
      110     120     130     140     150     160

      190     200     210     220     230     240
412  TTGTTGGCGAGGAGGGTAATGAGGAAGGACGAACACCTCACCTCCAGGGGTTGCTAATT
      ::::: ::::: ::::: ::::: ::::: :::::
PCV  TTTCGGGAGAGGAGGTTTGAAGAGGGTAGAACTCCTCACCTCCAGGGGTTTCCGAATT
      170     180     190     200     210     220

      250     260     270     280     290     300
412  TTGTGAAGAAGCAAACCTTTTAATAAAGTGAAGTGGTATTTGGGTGCCCGTGCCACATCG
      ::::: ::::: ::::: ::::: ::::: :::::
PCV  TTGCTAAGAAGCAGACTTTTAACAAGGTGAAGTGGTATTTGGGTGCCCGTGCCACATCG
      230     240     250     260     270     280

      310     320     330     340     350     360
412  AGAAAGCCAAAGGAACGTATCAGCAGAAATAAGAAATATTGCAGTAAAGAAGGCAACTTAC
      ::::: ::::: ::::: ::::: ::::: :::::
PCV  AGAAAGCGAAAGGAACCGACAGCAGAAATAAGAAATATTGCAGTAAAGAAGGCCACATAC
      290     300     310     320     330     340

      370     380     390     400     410     420
412  TTATTGAATGTGGAGCTCCTCGATCTCAAGGACAACGGAGTGACCTGTCTACTGCTGTGA
      ::::: ::::: ::::: ::::: ::::: :::::
PCV  TTATCGAGTGTGGAGCTCCCGGAACCGAGGGGAGCGCAGCGACCTGTCTACTGCTGTGA
      350     360     370     380     390     400

      430     440     450     460     470     480
412  GTACCTTGTGGAGAGCGGATTCGTGACCGTTGCAAGCAGCACCTGTAAACGTTTG
      ::::: ::::: ::::: ::::: ::::: :::::
PCV  GTACCCCTTTTGGAGACGGGTCTTTGGTGACTGTAGCCGAGCAGTTCCCTGTAAACGTATG
      410     420     430     440     450     460

      490     500     510     520     530     540
412  TCAAAAAATTCGCGGGCTGGCTGAACCTTTTGAAGTGAGCGGGAATGCAAAAGCGTG
      ::::: ::::: ::::: ::::: ::::: :::::
PCV  TGAGAAAATTCGCGGGCTGGCTGAACCTTTTGAAGTGAGCGGGAAGATGCAGCAGCGTG
      470     480     490     500     510     520

      550     560     570     580     590     600
412  ATTGGAAGAACCAATGTACACTTCATTGTGGGGCCACCTGGGTGTGGTAAAGCAAATGGG
      ::::: ::::: ::::: ::::: ::::: :::::
PCV  ATTGGAAGACAGCTGTACACGTATAGTGGGCCCCCGGTTGTGGGAAGAGCCAGTGGG
      530     540     550     560     570     580

```

50069233.121197

C9, SEQID No. 1

FIG. 4A



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.13 [Nov-27-2005]

Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☒ View option
Masking character option Masking color option
☐ Show CDS translation

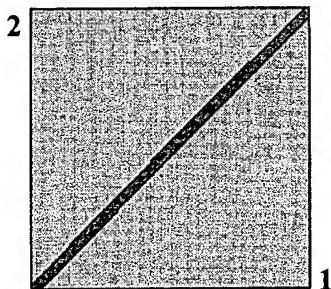
Sequence 1: lcl|seq_1
Length = 1767 (1 .. 1767)

DNA IS

JESTIN'S SEQ ID 15 v.
4/2 d'639

Sequence 2: lcl|seq_2
Length = 1768 (1 .. 1768)

422 seq 15/3 PTD WWW



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

Score = 2902 bits (1509), Expect = 0.0
Identities = 1688/1768 (95%), Gaps = 1/1768 (0%)
Strand=Plus/Plus

Query	1	ACCAGCGCACTTCGGCAGCGGCAGCACCTCGGCAGCACCTCAGCAGCAACATGCCCAGCA	60
Sbjct	1	ACCAGCGCACTTCGGCAGCGGCAGCACCTCGGCAGCACCTCAGCAGCAACATGCCCAGCA	60
Query	61	AGAAGAATGGAAGAAGCGGACCCCAACCCATAAAAGGTGGGTGTTCACTCTGAATAATC	120
Sbjct	61	AGAAGAATGGAAGAAGCGGACCCCAACACATAAAAGGTGGGTGTTCAAGCTGAATAATC	120
Query	121	CTTCCGAAGACGAGCGCAAGAAAATACGGGATCTTCCAATATCCCTATTTGATTATTTTA	180
Sbjct	121	CTTCCGAAGACGAGCGCAAGAAAATACGGGAGCTCCCAATCTCCCTATTTGATTATTTTA	180

Page 2 of 4

4/7/2006

Blast Result

Page 3 of 4

Query 1080 CATACATGGTTACACGGATATTGTATTCTGGTCGTATATACTGTTTTCGAACGCAGTGC 1139
|||||
Sbjct 1081 CATACATGGTTACACGGATATTGTAGTCCTGGTCGTATTTACTGTTTTCGAACGCAGTGC 1140

Query 1140 CGAGGCCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTTCTTT 1199
|||||
Sbjct 1141 CGAGGCCTACGTGGTCCACATTTCCAGAGGTTTGTAGCCTCAGCCAAAGCTGATTCTTTT 1200

Query 1200 TGTGTTTGGTTGGAAGTAATCAATAGTGAAATCTAGGACAGGTTTGGGGGTAAAGTACC 1259
|||||
Sbjct 1201 TGTATTTTGGTTGGAAGTAATCAATAGTGAGTCAAGAACAGGTTTGGGTGTGAAGTAAC 1260

Query 1260 GGGAGTGGTAGGAGAAGGGCTGGGTTATGGTATGGCGGGAGGAGTAGTTTACATAGGGGT 1319
|||||
Sbjct 1261 GGGAGTGGTAGGAGAAGGGTTGGGGGATTGTATGGCGGGAGGAGTAGTTTACATATGGGT 1320

Query 1320 CATAGGTGAGGGCTGTGGCCTTTGTTACAAAGTTATCATCTAAAATAACAGCACTGGAGC 1379
|||||
Sbjct 1321 CATAGGTTAGGGCTGTGGCCTTTGTTACAAAGTTATCATCTAAAATAACAGCAGTGGAGC 1380

Query 1380 CCACTCCCCGTGTCACCCTGGGTGATCGGGGAGCAGGGCCAGAATTC AACCTTAACCTTTC 1439
|||||
Sbjct 1381 CCACTCCCCATGTCACCCTGGGTGATGGGGGAGCAAGGCCAGAATTC AACCTTAACCTTTC 1440

Query 1440 TTATTCTGTAGTATTCAAAGGGCACAGAGCGGGGGTTTGACCCCCCTCCTGGGGGAAGAA 1499
|||||
Sbjct 1441 TTATTCTGTAGTATTCAAAGGGTATAGAGATTTTGTGGTCCCCCTCCCGGGGAACAA 1500

Query 1500 AGTCATTAATATTGAATCTCATCATGTCCACCGCCAGGAGGGCGTTCTGACTGTGGTTC 1559
|||||
Sbjct 1501 AGTCGTCAATTTTAAATCTCATCATGTCCACCGCCAGGAGGGCGTTCTGACTGTGGTAC 1560

Query 1560 GCTTGACAGTATATCCGAAGGTGCGGGAGAGGCGGGTGTGAAGATGCCATTTTTCCTTC 1619
|||||
Sbjct 1561 GCTTGACAGTATATCCGAAGGTGCGGGAGAGGCGGGTGTGAAGATGCCATTTTTCCTTC 1620

Query 1620 TCCAGCGGTAACGGTGGCGGGGTGGACGAGCCAGGGGCGGCGGCGGAGGATCTGGCCAA 1679
|||||
Sbjct 1621 TCCAACGGTAGCGGTGGCGGGGTGGACGAGCCAGGGGCGGCGGCGGAGGATCTGGCCAA 1680

Query 1680 GATGGCTGCGGGGGCGGTGTCTTCTTCTCGGTAACGCCTCCTTGGATACGTCATATCTG 1739
|||||
Sbjct 1681 GATGGCTGCGGGGGCGGTGTCTTCTTCTCGGTAACGCCTCCTTGGATACGTCATAGCTG 1740

Query 1740 AAAACGAAAGAAGTGCCTGTAAGTATT 1767
|||||
Sbjct 1741 AAAACGAAAGAAGTGCCTGTAAGTATT 1768

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda	K	H
1.33	0.621	1.12

Gapped		
Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 359
Number of extensions: 6
Number of successful extensions: 4
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 1767
Length of database: 16,974,423,555
Length adjustment: 27
Effective length of query: 1740
Effective length of database: 16,974,423,528
Effective search space: 29535496938720
Effective search space used: 29535496938720
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 14 (27.6 bits)
S2: 22 (43.0 bits)

**Blast 2 Sequences results**

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.13 [Nov-27-2005]

Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☒ View option
Masking character option ☒ X for protein, n for nucleotide Masking color option
☐ Show CDS translation

Sequence 1: lcl|seq_1
Length = 1767 (1 .. 1767)

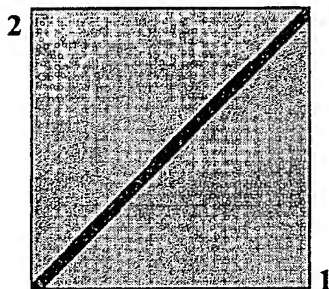
15

Sequence 2: lcl|seq_2
Length = 1768 (1 .. 1768)

412 fig

JESTIN'S SEQ ID 15 v.

412 d 1639 FIGURE



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

Score = 2896 bits (1506), Expect = 0.0
Identities = 1687/1768 (95%), Gaps = 1/1768 (0%)
Strand=Plus/Plus

Query	1	ACCAGCGCACTTCGGCAGCGGCAGCACCTCGGCAGCACCTCAGCAGCAACATGCCAGCA	60
Sbjct	1	ACCAGCGCACTTCGGCAGCGGCAGCACCTCGGCAGCACCTCAGCAGCAACATGCCAGCA	60
Query	61	AGAAGAATGGAAGAAGCGGACCCCAACCCATAAAAGGTGGGTGTTCACTCTGAATAATC	120
Sbjct	61	AGAAGAATGGAAGAAGCGGACCCCAACACATAAAAGGTGGGTGTTACAGCTGAATAATC	120
Query	121	CTTCCGAAGACGAGCGCAAGAAAATACGGGATCTTCCAATATCCCTATTGATTATTTTA	180
Sbjct	121	CTTCCGAAGACGAGCGCAAGAAAATACGGGAGCTCCCAATCTCCCTATTGATTATTTTA	180

```
Query 181 TTGTTGGCGAGGAGGGTAATGAGGAAGGACGAACACCTCACCTCCAGGGGTTTCGCTAATT 240
|||||
Sbjct 181 TTGTTGGCGAGGAGGGTAATGAGGAAGGACGAACACCTCACCTCCAGGGGTTTCGCTAATT 240

Query 241 TTGTGAAGAAGCAGACTTTTAATAAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG 300
|||||
Sbjct 241 TTGTGAAGAAGCAAACCTTTTAATAAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG 300

Query 301 AGAAAGCGAAAGGAACAGATCAGCAGAATAAAGAATACTGCAGTAAAGAAGGCAACTTAC 360
|||||
Sbjct 301 AGAAAGCCAAAGGAACCTGATCAGCAGAATAAAGAATATTGCAGTAAAGAAGGCAACTTAC 360

Query 361 TGATGGAGTGTGGAGCTCCTAGATCTCAGGGACAACGGAGTGACCTGTCTACTGCTGTGA 420
| || |
Sbjct 361 TTATTGAATGTGGAGCTCCTCGATCTCAAGGACAACGGAGCGACCTGTCTACTGCTGTGA 420

Query 421 GTACCTTGTGGAGAGCGGGAGTCTGGTGACCGTTGCAGAGCAGCACCCGTGAACGTTTG 480
|||||
Sbjct 421 GTACCTTGTGGAGAGCGGGATTCTGGTGACCGTTGCAAAGCAGCACCCGTGAACGTTTG 480

Query 481 TCAGAAATTTCCGCGGGGCTGGCTGAACCTTTTGAAAGTGAGCGGGAAAATGCAGAAGCGTG 540
||| |
Sbjct 481 TCAAAAATTTCCGCGGGGCTGGCTGAACCTTTTGAAAGTGAGCGGGAAAATGCAAAAGCGTG 540

Query 541 ATTGGAAGACTAATGTACACGTCATTGTGGGGCCACCTGGGTGTGGTAAAAGCAAATGGG 600
|||||
Sbjct 541 ATTGGAAGAAACCAATGTACACTTCATTGTGGGGCCACCTGGGTGTGGTAAAAGCAAATGGG 600

Query 601 CTGCTAATTTTGCAGACCCGGAACACATACTGGAAACCACCTAGAAAACAAGTGGTGGG 660
|||||
Sbjct 601 CTGCTAATTTTGCAAACCCGGAACACATACTGGAAACCACCTAAAAACAAGTGGTGGG 660

Query 661 ATGGTTACCATGGTGAAGAAGTGGTTGTTATTGATGACTTTTATGGCTGGCTGCCCTGGG 720
|||||
Sbjct 661 ATGGTTACCATGGTGAAAAAGTGGTTGTTATTGATGACTTTTATGGCTGGCTGCCCTGGG 720

Query 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAGAGACTAAAGGTGGAAGT 780
|||||
Sbjct 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAAAACTAAAGGTGGAAGT 780

Query 781 TACCTTTTTTGGCCCGCAGTATTCTGATTACCAGCAATCAGACCCCGTTGGAATGGTACT 840
|||||
Sbjct 781 TACCTTTTTTGGCCCGCAGTATTCTGATTACCAGCAATCAGACCCCGTTGGAATGGTACT 840

Query 841 CCTCAACTGCTGTCCCAGCTGTAGAAGCTCTTATCGGAGGATTACTTCCTTGGTATTTT 900
|||||
Sbjct 841 CCTCAACTGCTGTCCCAGCTGTAGAAGCTCTCTATCGGAGGATTACTTCCTTGGTATTTT 900

Query 901 GGAAGAATGCTACAGAACAATCCACGGAGGAAGGGGGCCAGTTCGTCACCCTTTnnnnnn 960
|||||
Sbjct 901 GGAAGAATGCTACAAAACAATCCACGGAGGAAGGGGGCCAGTTCGTCACCCTTTCCCCC 960

Query 961 nATGCCCTGAATTTCCATATGAAATAAATTACTGAGTCTTTTTTATCACTTCGTAATGGT 1020
|||||
Sbjct 961 CATGCCCTGAATTTCCATATGAAATAAATTACTGAGTCTTTTTTATCACTTCGTAATGGT 1020

Query 1021 TTTTATTATTCAATTAAGGGTT-AAGTGGGGGGCTTTAAAATTAAATTCTCTGAATTGTA 1079
|||||
Sbjct 1021 TTTTATTATTCAATTTAGGGTTCAAGTGGGGGGCTTTAAGATTAAATTCTCTGAATTGTA 1080
```

```

Query  1080  CATACATGGTTACACGGATATTGTATTCTGGTCGTATATACTGTTTTCGAACGCAGTGC  1139
          |||
Sbjct  1081  CATACATGGTTACACGGATATTGTAGTCCTGGTCGTATTTACTGTTTTCGAACGCAGTGC  1140

Query  1140  CGAGGCCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTTCTTT  1199
          |||
Sbjct  1141  CGAGGCCTACGTGGTCCACATTTCCAGAGGTTTGTAGCCTCAGCCAAAGCTGATTCCTTT  1200

Query  1200  TGTGTTTGGTTGGAAGTAATCAATAGTGAAATCTAGGACAGGTTTGGGGGTAAAGTACC  1259
          |||
Sbjct  1201  TGTATTTTGGTTGGAAGTAATCAATAGTGGAGTCAAGAACAGGTTTGGGTGTGAAGTAAC  1260

Query  1260  GGGAGTGGTAGGAGAAGGGCTGGGTTATGCTATGGCGGGAGGAGTAGTTTACATAGGGGT  1319
          |||
Sbjct  1261  GGGAGTGGTAGGAGAAGGGTTGGGGGATTGTATGGCGGGAGGAGTAGTTTACATATGGGT  1320

Query  1320  CATAGGTGAGGGCTGTGGCCTTTGTTACAAAGTTATCATCTAAAATAACAGCACTGGAGC  1379
          |||
Sbjct  1321  CATAGGTGAGGGCTGTGGCCTTTGTTACAAAGTTATCATCTAAAATAACAGCAGTGGAGC  1380

Query  1380  CCACTCCCCTGTCACCCTGGGTGATCGGGGAGCAGGGCCAGAATTCAACCTTAACCTTTC  1439
          |||
Sbjct  1381  CCACTCCCCATCACCTGGGTGATGGGGGAGCAAGGCCAGAATTCAACCTTAACCTTTC  1440

Query  1440  TTATTCTGTAGTATTCAAAGGGCACAGAGCGGGGGTTTGACCCCCCTCCTGGGGGAAGAA  1499
          |||
Sbjct  1441  TTATTCTGTAGTATTCAAAGGGTATAGAGATTTTGTGTTGGTCCCCCTCCCGGGGAACAA  1500

Query  1500  AGTCATTAATATTGAATCTCATCATGTCCACCGCCCAGGAGGGCGTTCTGACTGTGGTTC  1559
          |||
Sbjct  1501  AGTCGTCAATTTTAAATCTCATCATGTCCACCGCCCAGGAGGGCGTTGTGACTGTGGTAC  1560

Query  1560  GCTTGACAGTATATCCGAAGGTGCGGGAGAGGCGGGTGTTGAAGATGCCATTTTTCCTTC  1619
          |||
Sbjct  1561  GCTTGACAGTATATCCGAAGGTGCGGGAGAGGCGGGTGTTGAAGATGCCATTTTTCCTTC  1620

Query  1620  TCCAGCGGTAACGGTGGCGGGGGTGGACGAGCCAGGGGCGGCGGCGGAGGATCTGGCCAA  1679
          |||
Sbjct  1621  TCCAACGGTAGCGGTGGCGGGGGTGGACGAGCCAGGGGCGGCGGCGGAGGATCTGGCCAA  1680

Query  1680  GATGGCTGCGGGGGCGGTGTCTTCTTCTTCGGTAACGCCTCCTTGGATACGTCATATCTG  1739
          |||
Sbjct  1681  GATGGCTGCGGGGGCGGTGTCTTCTTCTGCGGTAACGCCTCCTTGGATACGTCATAGCTG  1740

Query  1740  AAAACGAAAGAAGTGCCTGTAAGTATT  1767
          |||
Sbjct  1741  AAAACGAAAGAAGTGCCTGTAAGTATT  1768

```

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 357
Number of extensions: 6
Number of successful extensions: 4
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 1767
Length of database: 16,974,423,555
Length adjustment: 27
Effective length of query: 1740
Effective length of database: 16,974,423,528
Effective search space: 29535496938720
Effective search space used: 29535496938720
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 14 (27.6 bits)
S2: 22 (43.0 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.13 [Nov-27-2005]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ View option
 Masking character option Masking color option
☐ Show CDS translation

Sequence 1: lc|seq_1
 Length = 1767 (1 .. 1767)

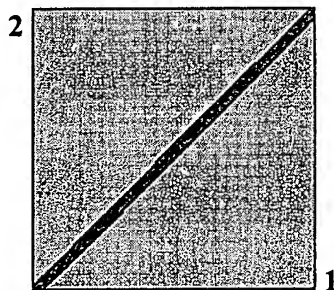
15

JESTINS' SEQ ID 15 v.

Sequence 2: lc|seq_2
 Length = 1768 (1 .. 1768)

412 Genbank

412 GENBANK d'639
 (AF085695)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

Score = 2902 bits (1509), Expect = 0.0
 Identities = 1688/1768 (95%), Gaps = 1/1768 (0%)
 Strand=Plus/Plus

Query	1	ACCAGCGCACTTCGGCAGCGGCAGCACCTTCGGCAGCACCTCAGCAGCAACATGCCCAGCA	60
Sbjct	1	ACCAGCGCACTTCGGCAGCGGCAGCACCTTCGGCAGCACCTCAGCAGCAACATGCCCAGCA	60
Query	61	AGAAGAATGGAAGAAGCGGACCCCAACCCATAAAAGGTGGGTGTTCACTCTGAATAATC	120
Sbjct	61	AGAAGAATGGAAGAAGCGGACCCCAACACATAAAAGGTGGGTGTTCACTCTGAATAATC	120
Query	121	CTTCCGAAGACGAGCGCAAGAAAATACGGGATCTTCCAATATCCCTATTTGATTATTTTA	180
Sbjct	121	CTTCCGAAGACGAGCGCAAGAAAATACGGGAGCTCCCAATCTCCCTATTTGATTATTTTA	180

Query 181 TTGTTGGCGAGGAGGGTAATGAGGAAGGACGAACACCTCACCTCCAGGGGTTTCGCTAATT 240
|||||
Sbjct 181 TTGTTGGCGAGGAGGGTAATGAGGAAGGACGAACACCTCACCTCCAGGGGTTTCGCTAATT 240

Query 241 TTGTGAAGAAGCAGACTTTTAATAAAGTGAAGTGGTATTTGGGTGCCCCGCTGCCACATCG 300
|||||
Sbjct 241 TTGTGAAGAAGCAAACCTTTTAATAAAGTGAAGTGGTATTTGGGTGCCCCGCTGCCACATCG 300

Query 301 AGAAAGCGAAAGGAACAGATCAGCAGAATAAAGAATACTGCAGTAAAGAAGGCAACTTAC 360
|||||
Sbjct 301 AGAAAGCCAAAGGAACCTGATCAGCAGAATAAAGAATATTGCAGTAAAGAAGGCAACTTAC 360

Query 361 TGATGGAGTGTGGAGCTCCTAGATCTCAGGGACAACGGAGTGACCTGTCTACTGCTGTGA 420
| || ||
Sbjct 361 TTATTGAATGTGGAGCTCCTCGATCTCAAGGACAACGGAGTGACCTGTCTACTGCTGTGA 420

Query 421 GTACCTTGTGGAGAGCGGGAGTCTGGTGACCGTTGCAGAGCAGCACCCCTGTAACGTTTG 480
|||||
Sbjct 421 GTACCTTGTGGAGAGCGGGATTCTGGTGACCGTTGCAAAGCAGCACCCCTGTAACGTTTG 480

Query 481 TCAGAAATTTCCGCGGGCTGGCTGAACCTTTTGAAAGTGAGCGGGAAAATGCAGAAGCGTG 540
||| ||
Sbjct 481 TCAAAAATTTCCGCGGGCTGGCTGAACCTTTTGAAAGTGAGCGGGAAAATGCAAAAGCGTG 540

Query 541 ATTGGAAGACTAATGTACACGTCATTGTGGGGCCACCTGGGTGTGGTAAAAGCAAATGGG 600
||||| ||
Sbjct 541 ATTGGAACCAATGTACACTTCATTGTGGGGCCACCTGGGTGTGGTAAAAGCAAATGGG 600

Query 601 CTGCTAATTTTGCAGACCCGGAACACATACTGGAACCCACCTAGAAACAAGTGGTGGG 660
|||||
Sbjct 601 CTGCTAATTTTGCAAACCCGGAACACATACTGGAACCCACCTAAAAACAAGTGGTGGG 660

Query 661 ATGGTTACCATGGTGAAGAAGTGGTTGTTATTGATGACTTTTATGGCTGGCTGCCCTGGG 720
|||||
Sbjct 661 ATGGTTACCATGGTGAAGAAGTGGTTGTTATTGATGACTTTTATGGCTGGCTGCCGTGGG 720

Query 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAGAGACTAAAGGTGGAAGT 780
|||||
Sbjct 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAAAAACTAAAGGTGGAAGT 780

Query 781 TACCTTTTTTGGCCCGCAGTATTCTGATTACCAGCAATCAGACCCCGTTGGAATGGTACT 840
|||||
Sbjct 781 TACCTTTTTTGGCCCGCAGTATTCTGATTACCAGCAATCAGACCCCGTTGGAATGGTACT 840

Query 841 CCTCAACTGCTGTCCCAGCTGTAGAAGCTCTTTATCGGAGGATTACTTCCTTGGTATTTT 900
|||||
Sbjct 841 CCTCAACTGCTGTCCCAGCTGTAGAAGCTCTCTATCGGAGGATTACTTCCTTGGTATTTT 900

Query 901 GGAAGAATGCTACAGAACAATCCACGGAGGAAGGGGGCCAGTTCGTCACCCCTTTnnnnnn 960
|||||
Sbjct 901 GGAAGAATGCTACAAAACAATCCACGGAGGAAGGGGGCCAGTTCGTCACCCCTTTCCCCC 960

Query 961 nATGCCCTGAATTTCCATATGAAATAAATTACTGAGTCTTTTTTATCACTTCGTAATGGT 1020
|||||
Sbjct 961 CATGCCCTGAATTTCCATATGAAATAAATTACTGAGTCTTTTTTATCACTTCGTAATGGT 1020

Query 1021 TTTTATTATTCAATTAAGGGTT-AAGTGGGGGTCTTTAAATTAATTTCTCTGAATTGTA 1079
|||||
Sbjct 1021 TTTTATTATTCAATTAAGGGTTCAAGTGGGGGTCTTTAAGATTAAATTTCTCTGAATTGTA 1080

```

Query  1080  CATACATGGTTACACGGATATTGTATTCCCTGGTCGTATATACTGTTTTCGAACGCAGTGC  1139
          |||
Sbjct  1081  CATACATGGTTACACGGATATTGTAGTCCTGGTCGTATTTACTGTTTTCGAACGCAGTGC  1140

Query  1140  CGAGGCCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTTCTTT  1199
          |||
Sbjct  1141  CGAGGCCTACGTGGTCCACATTTCCAGAGGTTGTAGCCTCAGCCAAAGCTGATTCTTTT  1200

Query  1200  TGTGTGTTTGGTTGGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACC  1259
          |||
Sbjct  1201  TGTATTTTGGTTGGAAGTAATCAATAGTGGAGTCAAGAACAGGTTTGGGTGTGAAGTAAC  1260

Query  1260  GGGAGTGGTAGGAGAAGGGCTGGGTTATGGTATGGCGGGAGGAGTAGTTTACATAGGGGT  1319
          |||
Sbjct  1261  GGGAGTGGTAGGAGAAGGGTTGGGGGATTGTATGGCGGGAGGAGTAGTTTACATATGGGT  1320

Query  1320  CATAGGTGAGGGCTGTGGCCTTTGTTACAAAGTTATCATCTAAAATAACAGCACTGGAGC  1379
          |||
Sbjct  1321  CATAGGTTAGGGCTGTGGCCTTTGTTACAAAGTTATCATCTAAAATAACAGCAGTGGAGC  1380

Query  1380  CCACTCCCCTGTCACCCTGGGTGATCGGGGAGCAGGGCCAGAATTCAACCTTAACCTTTC  1439
          |||
Sbjct  1381  CCACTCCCCTATCACCTGGGTGATGGGGGAGCAAGGCCAGAATTCAACCTTAACCTTTC  1440

Query  1440  TTATTCTGTAGTATTCAAAGGGCACAGAGCGGGGGTTTGACCCCCCTCCTGGGGGAAGAA  1499
          |||
Sbjct  1441  TTATTCTGTAGTATTCAAAGGGTATAGAGATTTTGTGGTCCCCCTCCCGGGGAACAA  1500

Query  1500  AGTCATTAATATTGAATCTCATCATGTCCACCGCCCAGGAGGGCGTTCTGACTGTGGTTC  1559
          |||
Sbjct  1501  AGTCGTCAATTTTAAATCTCATCATGTCCACCGCCCAGGAGGGCGTTGTGACTGTGGTAC  1560

Query  1560  GCTTGACAGTATATCCGAAGGTGCGGGAGAGGCGGGTGTGAAGATGCCATTTTTCCTTC  1619
          |||
Sbjct  1561  GCTTGACAGTATATCCGAAGGTGCGGGAGAGGCGGGTGTGAAGATGCCATTTTTCCTTC  1620

Query  1620  TCCAGCGGTAACGGTGGCGGGGTGGACGAGCCAGGGGCGGCGGCGGAGGATCTGGCCAA  1679
          |||
Sbjct  1621  TCCAACGGTAGCGGTGGCGGGGTGGACGAGCCAGGGGCGGCGGCGGAGGATCTGGCCAA  1680

Query  1680  GATGGCTGCGGGGGCGGTGTCTTCTTCTTCGGTAACGCCTCCTTGGATACGTCATATCTG  1739
          |||
Sbjct  1681  GATGGCTGCGGGGGCGGTGTCTTCTTCTGCGGTAACGCCTCCTTGGATACGTCATAGCTG  1740

Query  1740  AAAACGAAAGAAGTGCCTGTAAGTATT  1767
          |||
Sbjct  1741  AAAACGAAAGAAGTGCCTGTAAGTATT  1768

```

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total secs.

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

1
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 359
Number of extensions: 6
Number of successful extensions: 4
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 1767
Length of database: 16,974,423,555
Length adjustment: 27
Effective length of query: 1740
Effective length of database: 16,974,423,528
Effective search space: 29535496938720
Effective search space used: 29535496938720
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 14 (27.6 bits)
S2: 22 (43.0 bits)

**Blast 2 Sequences results**

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.13 [Nov-27-2005]

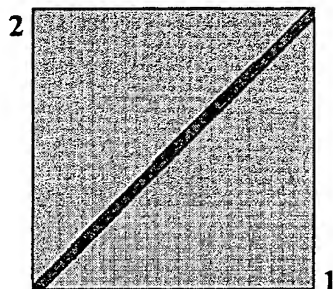
Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☒ View option
Masking character option Masking color option
☐ Show CDS translation

Sequence 1: lcl|seq_1
Length = 1767 (1 .. 1767)

15 JESTIN'S SEQ ID 15 v.
9741d'639

Sequence 2: lcl|seq_2
Length = 1768 (1 .. 1768)

9741 whw



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

Score = 2896 bits (1506), Expect = 0.0
Identities = 1687/1768 (95%), Gaps = 1/1768 (0%)
Strand=Plus/Plus

Query	1	ACCAGCGCACTTCGGCAGCGGCAGCACCTCGGCAGCACCTCAGCAGCAACATGCCCAGCA	60
Sbjct	1	ACCAGCGCACTTCGGCAGCGGCAGCACCTCGGCAGCACCTCAGCAGCAACATGCCCAGCA	60
Query	61	AGAAGAATGGAAGAAGCGGACCCCAACCCATAAAAGGTGGGTGTTCACTCTGAATAATC	120
Sbjct	61	AGAAGAATGGAAGAAGCGGACCCCAACCCATAAAAGGTGGGTGTTCACTCTGAATAATC	120
Query	121	CTTCCGAAGACGAGCGCAAGAAAATACGGGATCTTCCAATATCCCTATTTGATTATTTTA	180
Sbjct	121	CTTCCGAAGACGAGCGCAAGAAAATACGGGATCTTCCAATATCCCTATTTGATTATTTTA	180

Query 181 TTGTTGGCGAGGAGGGTAATGAGGAAGGACGAACACCTCACCTCCAGGGGTTCGCTAATT 240
|||||
Sbjct 181 TTGTTGGCGAGGAGGGTAATGAGGAAGGACGAACACCTCACCTCCAGGGGTTCGCTAATT 240

Query 241 TTGTGAAGAAGCAGACTTTTAATAAAGTGAAGTGGTATTTGGGTGCCCCTGCCACATCG 300
|||||
Sbjct 241 TTGTGAAGAAGCAAACCTTTTAATAAAGTGAAGTGGTATTTGGGTGCCCCTGCCACATCG 300

Query 301 AGAAAGCGAAAGGAACAGATCAGCAGAATAAAGAATACTGCAGTAAAGAAGGCAACTTAC 360
|||||
Sbjct 301 AGAAAGCCAAAGGAACCTGATCAGCAGAATAAAGAATATTGCAGTAAAGAAGGCAACTTAC 360

Query 361 TGATGGAGTGTGGAGCTCCTAGATCTCAGGGACAACGGAGTGACCTGTCTACTGCTGTGA 420
|||
Sbjct 361 TTATTGAATGTGGAGCTCCTCGATCTCAAGGACAACGGAGTGACCTGTCTACTGCTGTGA 420

Query 421 GTACCTTGTGGAGAGCGGGAGTCTGGTGACCGTTGCAGAGCAGCACCCCTGTAACGTTTG 480
|||||
Sbjct 421 GTACCTTGTGGAGAGCGGGATTCTGGTGACCGTTGCAAAGCAGCACCCCTGTAACGTTTG 480

Query 481 TCAGAAATTTCCGCGGGCTGGCTGAACCTTTTGAAAGTGAGCGGAAAATGCAGAAGCGTG 540
|||
Sbjct 481 TCAAAATTTCCGCGGGCTGGCTGAACCTTTTGAAAGTGAGCGGAAAATGCAAAGCGTG 540

Query 541 ATTGGAAGACTAATGTACACGTCATTGTGGGGCCACCTGGGTGTGGTAAAAGCAAATGGG 600
|||||
Sbjct 541 ATTGGAAGAAACCAATGTACACTTCATTGTGGGGCCACCTGGGTGTGGTAAAAGCAAATGGG 600

Query 601 CTGCTAATTTTGCAGACCCGGAACACATACTGGAACACCTAGAAACAAGTGGTGGG 660
|||||
Sbjct 601 CTGCTAATTTTGCAGACCCGGAACACATACTGGAACACCTAGAAACAAGTGGTGGG 660

Query 661 ATGGTTACCATGGTGAAGAAGTGGTTGTTATTGATGACTTTTATGGCTGGCTGCCCTGGG 720
|||||
Sbjct 661 ATGGTTACCATGGTGAAGAAGTGGTTGTTATTGATGACTTTTATGGCTGGCTGCCCTGGG 720

Query 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAGAGACTAAAGGTGGAAGT 780
|||||
Sbjct 721 ATGATCTACTGAAACTGTGTGATCGATATCCATTGACTGTAAAGTAAAGGTGGAAGT 780

Query 781 TACCTTTTTTGGCCCGCAGTATTCTGATTACCAGCAATCAGACCCCGTTGGAATGGTACT 840
|||||
Sbjct 781 TACCTTTTTTGGCCCGCAGTATTCTGATTACCAGCAATCAGACCCCGTTGGAATGGTACT 840

Query 841 CCTCAACTGCTGTCCAGCTGTAGAAGCTCTTTATCGGAGGATTACTTCCTTGGTATTTT 900
|||||
Sbjct 841 CCTCAACTGCTGTCCAGCTGTAGAAGCTCTTATCGGAGGATTACTTCCTTGGTATTTT 900

Query 901 GGAAGAATGCTACAGAACAATCCACGGAGGAAGGGGGCCAGTTCGTCACCCCTTTnnnnnn 960
|||||
Sbjct 901 GGAAGAATGCTACAGAACAATCCACGGAGGAAGGGGGCCAGTTTGTACCCCTTTCCCCC 960

Query 961 nATGCCCTGAATTTCCATATGAAATAAATTACTGAGTCTTTTTTATCACTTCGTAATGGT 1020
|||||
Sbjct 961 CATGCCCTGAATTTCCATATGAAATAAATTACTGAGTCTTTTTTATCACTTCGTAATGGT 1020

Query 1021 TTTTATTATTCATTAAGGG-TTAAGTGGGGGTCTTTAAATTAATTCTCTGAATTGTA 1079
|||||
Sbjct 1021 TTTTATTATTCATTTAGGGTTTAAGTGGGGGTCTTTAAGATTAAATTCTCTGAATTGTA 1080

Blast Result

Page 3 of 4

```

Query  1080  CATACATGGTTACACGGATATTGTATTCTGGTTCGTATATACTGTTTTCGAACGCAGTGC  1139
          |||
Sbjct  1081  CATACATGGTTACACGGATATTGTAGTCTGGTTCGTATTTACTGTTTTCGAACGCAGTGC  1140

Query  1140  CGAGGCCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTTCTTT  1199
          |||
Sbjct  1141  CGAGGCCTACGTGGTCCACATTTCCAGAGGTTTGTAGCCTCAGCCAAAGCTGATTCTTT  1200

Query  1200  TGTGTTTTGGTTGGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACC  1259
          |||
Sbjct  1201  TGTATTTGGTTGGAAGTAATCAATAGTGGAGTCAAGAACAGGTTTGGGTGTGAAGTAAC  1260

Query  1260  GGGAGTGGTAGGAGAAGGGCTGGGTTATGGTATGGCGGGAGGAGTAGTTACATAGGGGT  1319
          |||
Sbjct  1261  GGGAGTGGTAGGAGAAGGGTTGGGGGATTGTATGGCGGGAGGAGTAGTTACATATGGGT  1320

Query  1320  CATAGGTGAGGGCTGTGGCCTTTGTTACAAAGTTATCATCTAAAATAACAGCACTGGAGC  1379
          |||
Sbjct  1321  CATAGGTTAGGGCTGTGGCCTTTGTTACAAAGTTATCATCTAAAATAACAGCAGTGGAGC  1380

Query  1380  CCACTCCCCTGTCACCCTGGGTGATCGGGGAGCAGGGCCAGAATTCAACCTTAACCTTTC  1439
          |||
Sbjct  1381  CCACTCCCCTATCACCTGGGTGATGGGGGAGCAGGGCCAGAATTCAACCTTAACCTTTC  1440

Query  1440  TTATTCTGTAGTATTCAAAGGGCACAGAGCGGGGGTTTGACCCCCCTCTGGGGGAAGAA  1499
          |||
Sbjct  1441  TTATTCTGTAGTATTCAAAGGGTATAGAGATTTTGTGGTCCCCCTCCCGGGGAACAA  1500

Query  1500  AGTCATTAATATTGAATCTCATCATGTCCACCGCCCAGGAGGGCGTTCTGACTGTGGTTC  1559
          |||
Sbjct  1501  AGTCGTCAATTTTAAATCTCATCATGTCCACCGCCCAGGAGGGCGTTGTGACTGTGGTAC  1560

Query  1560  GCTTGACAGTATATCCGAAGGTGCGGGAGAGGCGGGTGTTGAAGATGCCATTTTCTTTC  1619
          |||
Sbjct  1561  GCTTGACAGTATATCCGAAGGTGCGGGAGAGGCGGGTGTTGAAGATGCCATTTTCTTTC  1620

Query  1620  TCCAGCGGTAACGGTGGCGGGGGTGGACGAGCCAGGGGCGGCGGCGGAGGATCTGGCCAA  1679
          |||
Sbjct  1621  TCCAACGGTAGCGGTGGCGGGGGTGGACGAGCCAGGGGCGGCGGCGGAGGATCTGGCCAA  1680

Query  1680  GATGGCTGCGGGGGCGGTGTCTTCTTCTCGGTAACGCCTCCTTGGATACGTCATATCTG  1739
          |||
Sbjct  1681  GATGGCTGCGGGGGCGGTGTCTTCTTCTGCGGTAACGCCTCCTTGGATACGTCATAGCTG  1740

Query  1740  AAAACGAAAGAAGTGCCTGTAAGTATT  1767
          |||
Sbjct  1741  AAAACGAAAGAAGTGCCTGTAAGTATT  1768

```

CPU time: 0.02 user secs. 0.02 sys. secs 0.04 total secs.

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 358
Number of extensions: 6
Number of successful extensions: 4
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 1767
Length of database: 16,974,423,555
Length adjustment: 27
Effective length of query: 1740
Effective length of database: 16,974,423,528
Effective search space: 29535496938720
Effective search space used: 29535496938720
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 14 (27.6 bits)
S2: 22 (43.0 bits)

**Blast 2 Sequences results**

PubMed

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BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.13 [Nov-27-2005]

Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☒ View option
Masking character option Masking color option
☐ Show CDS translation

Sequence 1: lcl|seq_1
Length = 1768 (1 .. 1768)

9741 mb-h

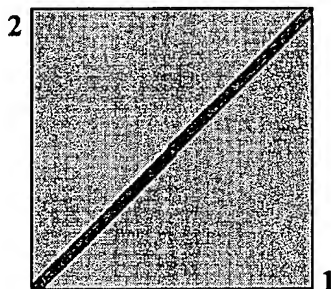
9741 d GENBANK d '639 v.

← AF086835

Sequence 2: lcl|seq_2
Length = 1768 (1 .. 1768)

9741 PTO seq

9741 d '639



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

Score = 3355 bits (1745), Expect = 0.0
Identities = 1765/1768 (99%), Gaps = 0/1768 (0%)
Strand=Plus/Plus

Query	1	ACCAGCGCACTTCGGCAGCGGCAGCACCTCGGCAGCACCTCAGCAGCAACATGCCCAGCA	60
Sbjct	1	ACCAGCGCACTTCGGCAGCGGCAGCACCTCGGCAGCACCTCAGCAGCAACATGCCCAGCA	60
Query	61	AGAAGAATGGAAGAAGCGGACCCCAACCACATAAAAGGTGGGTGTTACGCTGAATAATC	120
Sbjct	61	AGAAGAATGGAAGAAGCGGACCCCAACCACATAAAAGGTGGGTGTTACGCTGAATAATC	120
Query	121	CTTCCGAAAACAAGCGCAAGAAAATACGGGAGCTCCCAATCTCCCTATTTGATTATTTTA	180
Sbjct	121	CTTCCGAAGACAAGCGCAAGAAAATACGGGAGCTCCCAATCTCCCTATTTGATTATTTTA	180

↑
PTO

```
Query 181 TTGTTGGCGAGGAGGGTAATGAGGAAGGACGAACACCTCACCTCCAGGGGTTCGCTAATT 240
|||||
Sbjct 181 TTGTTGGCGAGGAGGGTAATGAGGAAGGACGAACACCTCACCTCCAGGGGTTCGCTAATT 240

Query 241 TTGTGAAGAAGCAAACCTTTTAATAAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG 300
|||||
Sbjct 241 TTGTGAAGAAGCAAACCTTTTAATAAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG 300

Query 301 AGAAAGCCAAAGGAACTGATCAGCAAAAATAAAGAATATTGCAGTAAAGAAGGCAACTTAC 360
|||||
Sbjct 301 AGAAAGCCAAAGGAACTGATCAGCAGAATAAAGAATATTGCAGTAAAGAAGGCAACTTAC 360

Query 361 TTATTGAATGTGGAGCTCCTCGATCTCAAGGACAACGGAGTGACCTGTCTACTGCTGTGA 420
|||||
Sbjct 361 TTATTGAATGTGGAGCTCCTCGATCTCAAGGACAACGGAGTGACCTGTCTACTGCTGTGA 420

Query 421 GTACCTTGTGGAGAGCGGGATTCTGGTGACCGTTGCAAAGCAGCACCTGTAACGTTTG 480
|||||
Sbjct 421 GTACCTTGTGGAGAGCGGGATTCTGGTGACCGTTGCAAAGCAGCACCTGTAACGTTTG 480

Query 481 TCAAAAATTTCCGCGGGCTGGCTGAACCTTTTGAAAGTGAGCGGGAAAATGCAAAGCGTG 540
|||||
Sbjct 481 TCAAAAATTTCCGCGGGCTGGCTGAACCTTTTGAAAGTGAGCGGGAAAATGCAAAGCGTG 540

Query 541 ATTGGAAAACCAATGTACACTTCATTGTGGGGCCACCTGGGTGTGGTAAAAGCAAATGGG 600
|||||
Sbjct 541 ATTGGAAAACCAATGTACACTTCATTGTGGGGCCACCTGGGTGTGGTAAAAGCAAATGGG 600

Query 601 CTGCTAATTTTGCAAACCCGGAACACATACTGGAACACCTAAAAACAAGTGGTGGG 660
|||||
Sbjct 601 CTGCTAATTTTGCAAACCCGGAACACATACTGGAACACCTAAAAACAAGTGGTGGG 660

Query 661 ATGGTTACCATGGTGAAAAAGTGGTTGTTATTGATGACTTTTATGGCTGGCTGCCGTGGG 720
|||||
Sbjct 661 ATGGTTACCATGGTGAAAAAGTGGTTGTTATTGATGACTTTTATGGCTGGCTGCCGTGGG 720

Query 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAAAACTAAAGGTGGAAGT 780
|||||
Sbjct 721 ATGATCTACTGAAACTGTGTGATCGATATCCATTGACTGTAAAACTAAAGGTGGAAGT 780

Query 781 TACCTTTTTTGGCCCGCAGTATTCTGATTACCAGCAATCAGACCCCGTTGGAATGGTACT 840
|||||
Sbjct 781 TACCTTTTTTGGCCCGCAGTATTCTGATTACCAGCAATCAGACCCCGTTGGAATGGTACT 840

Query 841 CCTCAACTGCTGTCCAGCTGTAGAAGCTCTCTATCGGAGGATTACTTCCTTGGTATTTT 900
|||||
Sbjct 841 CCTCAACTGCTGTCCAGCTGTAGAAGCTCTCTATCGGAGGATTACTTCCTTGGTATTTT 900

Query 901 GGAAGAATGCTACAGAACAATCCACGGAGGAAGGGGGCCAGTTTGTACCCTTTnnnnnn 960
|||||
Sbjct 901 GGAAGAATGCTACAGAACAATCCACGGAGGAAGGGGGCCAGTTTGTACCCTTTCCCCC 960

Query 961 nATGCCCTGAATTTCCATATGAAATAAATTACTGAGTCTTTTTTATCACTTCGTAATGGT 1020
|||||
Sbjct 961 CATGCCCTGAATTTCCATATGAAATAAATTACTGAGTCTTTTTTATCACTTCGTAATGGT 1020

Query 1021 TTTTATTATTCATTTAGGGTTTAAGTGGGGGGTCTTTAAGATTAAATTCTCTGAATTGTA 1080
|||||
Sbjct 1021 TTTTATTATTCATTTAGGGTTTAAGTGGGGGGTCTTTAAGATTAAATTCTCTGAATTGTA 1080
```

```

Query 1081  CATACATGGTTACACGGATATTGTAGTCCTGGTCGTATTTACTGTTTTCGAACGCAGTGC 1140
           |||
Sbjct 1081  CATACATGGTTACACGGATATTGTAGTCCTGGTCGTATTTACTGTTTTCGAACGCAGTGC 1140

Query 1141  CGAGGCCTACGTGGTCCACATTTCCAGAGGTTTGTAGCCTCAGCCAAAGCTGATTCCCTTT 1200
           |||
Sbjct 1141  CGAGGCCTACGTGGTCCACATTTCCAGAGGTTTGTAGCCTCAGCCAAAGCTGATTCCCTTT 1200

Query 1201  TGTTATTTGGTTGGAAGTAATCAATAGTGGAGTCAAGAACAGGTTTGGGTGTGAAGTAAC 1260
           |||
Sbjct 1201  TGTTATTTGGTTGGAAGTAATCAATAGTGGAGTCAAGAACAGGTTTGGGTGTGAAGTAAC 1260

Query 1261  GGGAGTGGTAGGAGAAGGGTTGGGGGATTGTATGGCGGGAGGAGTAGTTTACATATGGGT 1320
           |||
Sbjct 1261  GGGAGTGGTAGGAGAAGGGTTGGGGGATTGTATGGCGGGAGGAGTAGTTTACATATGGGT 1320

Query 1321  CATAGGTTAGGGCTGTGGCCTTTGTTACAAAGTTATCATCTAAAATAACAGCAGTGGAGC 1380
           |||
Sbjct 1321  CATAGGTTAGGGCTGTGGCCTTTGTTACAAAGTTATCATCTAAAATAACAGCAGTGGAGC 1380

Query 1381  CCACTCCCTATCACCTGGGTGATGGGGGAGCAGGGCCAGAAATCAACCTTAACCTTTC 1440
           |||
Sbjct 1381  CCACTCCCTATCACCTGGGTGATGGGGGAGCAGGGCCAGAAATCAACCTTAACCTTTC 1440

Query 1441  TTATTCTGTAGTATTCAAAGGGTATAGAGATTTTGTGGTCCCCCTCCCGGGGAACAA 1500
           |||
Sbjct 1441  TTATTCTGTAGTATTCAAAGGGTATAGAGATTTTGTGGTCCCCCTCCCGGGGAACAA 1500

Query 1501  AGTCGTCAATTTTAAATCTCATCATGTCCACCGCCCAGGAGGGCGTTGTGACTGTGGTAC 1560
           |||
Sbjct 1501  AGTCGTCAATTTTAAATCTCATCATGTCCACCGCCCAGGAGGGCGTTGTGACTGTGGTAC 1560

Query 1561  GCTTGACAGTATATCCGAAGGTGCGGGAGAGGCGGGTGTGAAGATGCCATTTTTCCTTC 1620
           |||
Sbjct 1561  GCTTGACAGTATATCCGAAGGTGCGGGAGAGGCGGGTGTGAAGATGCCATTTTTCCTTC 1620

Query 1621  TCCAACGGTAGCGGTGGCGGGGGTGGACGAGCCAGGGGCGGCGGCGGAGGATCTGGCCAA 1680
           |||
Sbjct 1621  TCCAACGGTAGCGGTGGCGGGGGTGGACGAGCCAGGGGCGGCGGCGGAGGATCTGGCCAA 1680

Query 1681  GATGGCTGCGGGGGCGGTGTCTTCTTCTGCGGTAACGCCTCCTTGGATACGTCATAGCTG 1740
           |||
Sbjct 1681  GATGGCTGCGGGGGCGGTGTCTTCTTCTGCGGTAACGCCTCCTTGGATACGTCATAGCTG 1740

Query 1741  AAAACGAAAGAAGTGCCTGTAAGTATT 1768
           |||
Sbjct 1741  AAAACGAAAGAAGTGCCTGTAAGTATT 1768

```

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 470
Number of extensions: 5
Number of successful extensions: 3
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 1768
Length of database: 16,974,423,555
Length adjustment: 27
Effective length of query: 1741
Effective length of database: 16,974,423,528
Effective search space: 29552471362248
Effective search space used: 29552471362248
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 14 (27.6 bits)
S2: 22 (43.0 bits)

**Blast 2 Sequences results**

PubMed

Entrez

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Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.13 [Nov-27-2005]

Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☒ View option
Masking character option ☒ X for protein, n for nucleotide Masking color option
☐ Show CDS translation

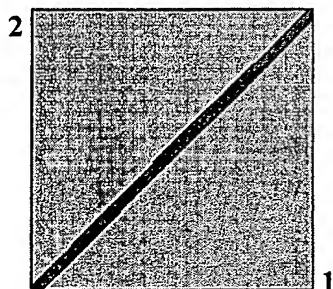
Sequence 1: lcl|seq_1
Length = 1767 (1 .. 1767)

15 Justin's SEQ ID 15 v.

Sequence 2: lcl|412Figure
Length = 1768 (1 .. 1768)

9741 Figure

9741 FIGURE d '639



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

Score = 2878 bits (1497), Expect = 0.0
Identities = 1684/1768 (95%), Gaps = 1/1768 (0%)
Strand=Plus/Plus

Query	1	ACCAGCGCACTTCGGCAGCGGCAGCACCTCGGCAGCACCTCAGCAGCAACATGCCCAGCA	60
Sbjct	1	ACCAGCGCACTTCGGCAGCGGCAGCACCTCGGCAGCACCTCAGCAGCAACATGCCCAGCA	60
Query	61	AGAAGAATGGAAGAAGCGGACCCCAACCCATAAAAGGTGGGTGTTCACTCTGAATAATC	120
Sbjct	61	AGAAGAATGGAAGAAGCGGACCCCAACCCATAAAAGGTGGGTGTTCACTCTGAATAATC	120
Query	121	CTTCCGAAGACGAGCGCAAGAAAATACGGGATCTTCCAATATCCCTATTGATTATTTTA	180
Sbjct	121	CTTCCGAAGACGAGCGCAAGAAAATACGGGATCTTCCAATATCCCTATTGATTATTTTA	180

```
Query 181 TTGTTGGCGAGGAGGGTAATGAGGAAGGACGAACACCTCACCTCCAGGGGTTGCTAATT 240
          |||
Sbjct 181 TTGTTGGCGAGGAGGGTAATGAGGAAGGACGAACACCTCACCTCCAGGGGTTGCTAATT 240

Query 241 TTGTGAAGAAGCAGACTTTTAATAAAGTGAAGTGGTATTTGGGTGCCCCTGCCACATCG 300
          |||
Sbjct 241 TTGTGAAGAAGCAAACCTTTTAATAAAGTGAAGTGGTATTTGGGTGCCCCTGCCACATCG 300

Query 301 AGAAAGCGAAAGGAACAGATCAGCAGAATAAAGAATACTGCAGTAAAGAAGGCAACTTAC 360
          |||
Sbjct 301 AGAAAGCGAAAGGAACACTGATCAGCAAAATAAAGAATATTGCAGTAAAGAAGGCAACTTAC 360

Query 361 TGATGGAGTGTGGAGCTCCTAGATCTCAGGGACAACGGAGTGACCTGTCTACTGCTGTGA 420
          |||
Sbjct 361 TTATTGAATGTGGAGCTCCTCGATCTCAAGGACAACGGAGCGACCTGTCTACTGCTGTGA 420

Query 421 GTACCTTGTGGAGAGCGGGAGTCTGGTGACCGTTGCAGAGCAGCACCCCTGTAACGTTTG 480
          |||
Sbjct 421 GTACCTTGTGGAGAGCGGGATTCTGGTGACCGTTGCAAAGCAGCACCCCTGTAACGTTTG 480

Query 481 TCAGAAATTTCCGCGGGCTGGCTGAACCTTTTGAAAGTGAGCGGGAAAATGCAGAAGCGTG 540
          |||
Sbjct 481 TCAAAATTTCCGCGGGCTGGCTGAACCTTTTGAAAGTGAGCGGGAAAATGCAAAGCGTG 540

Query 541 ATTGGAAGACTAATGTACACGTCATTGTGGGGCCACCTGGGTGTGGTAAAAGCAAATGGG 600
          |||
Sbjct 541 ATTGGAAGAACCAATGTACACTTCATTGTGGGGCCACCTGGGTGTGGTAAAAGCAAATGGG 600

Query 601 CTGCTAATTTTGCAGACCCGGAACACATACTGGAACACCTAGAAACAAGTGGTGGG 660
          |||
Sbjct 601 CTGCTAATTTTGCAGACCCGGAACACATACTGGAACACCTAGAAACAAGTGGTGGG 660

Query 661 ATGGTTACCATGGTGAAGAAGTGGTTGTTATTGATGACTTTTATGGCTGGCTGCCCTGGG 720
          |||
Sbjct 661 ATGGTTACCATGGTGAAGAAGTGGTTGTTATTGATGACTTTTATGGCTGGCTGCCCTGGG 720

Query 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAGAGACTAAAGGTGGAAGT 780
          |||
Sbjct 721 ATGATCTACTGAAACTGTGTGATCGATATCCATTGACTGTAAAGTAAAGGTGGAAGT 780

Query 781 TACCTTTTTTGGCCCGCAGTATTCTGATTACCAGCAATCAGACCCCGTTGGAATGGTACT 840
          |||
Sbjct 781 TACCTTTTTTGGCCCGCAGTATTCTGATTACCAGCAATCAGACCCCGTTGGAATGGTACT 840

Query 841 CCTCAACTGCTGTCCAGCTGTAGAAGCTCTTTATCGGAGGATTACTTCCTTGGTATTTT 900
          |||
Sbjct 841 CCTCAACTGCTGTCCAGCTGTAGAAGCTCTTATCGGAGGATTACTTCCTTGGTATTTT 900

Query 901 GGAAGAATGCTACAGAACAATCCACGGAGGAAGGGGGCCAGTTCGTCACCCCTTTnnnnnn 960
          |||
Sbjct 901 GGAAGAATGCTACAAAACAATCCACGGAGGAAGGGGGCCAGTTTGTACCCCTTTCCCCC 960

Query 961 nATGCCCTGAATTTCCATATGAAATAAATTACTGAGTCTTTTTTATCACTTCGTAATGGT 1020
          |||
Sbjct 961 CATGCCCTGAATTTCCATATGAAATAAATTACTGAGTCTTTTTTATCACTTCGTAATGGT 1020

Query 1021 TTTTATTATTTCATTAAGGG-TTAAGTGGGGGTCTTTAAAATTAAATTCTCTGAATTGTA 1079
          |||
Sbjct 1021 TTTTATTATTTCATTTAGGGTTTAAGTGGGGGTCTTTAAGATTAAATTCTCTGAATTGTA 1080
```

```

Query 1080  CATACATGGTTACACGGATATTGTATTCCTGGTTCGTATATACTGTTTTCGAACGCAGTGC 1139
          |||
Sbjct 1081  CATACATGGTTACACGGATATTGTAGTCCTGGTTCGTATTTACTGTTTTCGAACGCAGTGC 1140

Query 1140  CGAGGCCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTTCTTT 1199
          |||
Sbjct 1141  CGAGGCCTACGTGGTCCACATTTCCAGAGGTTGTAGCCTCAGCCAAAGCTGATTCCTTT 1200

Query 1200  TGTGTGTTTGGTTGGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACC 1259
          |||
Sbjct 1201  TGTATTTGGTTGGAAGTAATCAATAGTGGAGTCAAGAACAGGTTTGGGTGTGAAGTAAC 1260

Query 1260  GGGAGTGGTAGGAGAAGGGCTGGGTTATGGTATGGCGGGAGGAGTAGTTACATAGGGGT 1319
          |||
Sbjct 1261  GGGAGTGGTAGGAGAAGGGTTGGGGGATTGTATGGCGGGAGGAGTAGTTACATATGGGT 1320

Query 1320  CATAGGTGAGGGCTGTGGCCTTTGTTACAAAGTTATCATCTAAAATAACAGCACTGGAGC 1379
          |||
Sbjct 1321  CATAGGTTAGGGCTGTGGCCTTTGTTACAAAGTTATCATCTAAAATAACAGCAGTGGAGC 1380

Query 1380  CCACTCCCCTGTCACCCTGGGTGATCGGGGAGCAGGGCCAGAATTCAACCTTAACCTTTC 1439
          |||
Sbjct 1381  CCACTCCCCTATCACCTGGGTGATGGGGGAGCAGGGCCAGAATTCAACCTTAACCTTTC 1440

Query 1440  TTATTCTGTAGTATTCAAAGGGCACAGAGCGGGGTTTGACCCCCCTCCTGGGGGAAGAA 1499
          |||
Sbjct 1441  TTATTCTGTAGTATTCAAAGGGTATAGAGATTTGTTGGTCCCCCTCCGGGGGAACAA 1500

Query 1500  AGTCATTAATATTGAATCTCATCATGTCCACCGCCCAGGAGGGCGTTCTGACTGTGGTTC 1559
          |||
Sbjct 1501  AGTCGTCAATTTTAAATCTCATCATGTCCACCGCCCAGGAGGGCGTTGTGACTGTGGTAC 1560

Query 1560  GCTTGACAGTATATCCGAAGGTGCGGGAGAGGCGGGTGTTGAAGATGCCATTTTCCTTC 1619
          |||
Sbjct 1561  GCTTGACAGTATATCCGAAGGTGCGGGAGAGGCGGGTGTTGAAGATGCCATTTTCCTTC 1620

Query 1620  TCCAGCGGTAACGGTGGCGGGGTGGACGAGCCAGGGGCGGCGGCGGAGGATCTGGCCAA 1679
          |||
Sbjct 1621  TCCAACGGTAGCGGTGGCGGGGTGGACGAGCCAGGGGCGGCGGCGGAGGATCTGGCCAA 1680

Query 1680  GATGGCTGCGGGGCGGTGTCTTCTTCTCGGTAACGCCTCCTTGGATACGTCATATCTG 1739
          |||
Sbjct 1681  GATGGCTGCGGGGCGGTGTCTTCTTCTGCGGTAACGCCTCCTTGGATACGTCATAGCTG 1740

Query 1740  AAAACGAAAGAAGTGCCTGTAAGTATT 1767
          |||
Sbjct 1741  AAAACGAAAGAAGTGCCTGTAAGTATT 1768

```

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 352
Number of extensions: 6
Number of successful extensions: 4
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 1767
Length of database: 16,974,423,555
Length adjustment: 27
Effective length of query: 1740
Effective length of database: 16,974,423,528
Effective search space: 29535496938720
Effective search space used: 29535496938720
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 14 (27.6 bits)
S2: 22 (43.0 bits)



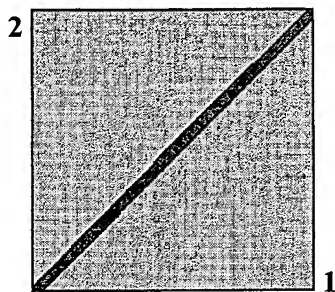
Structure

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ View option
 Masking character option Masking color option
☐ Show CDS translation

15 JESTINE'S SEQ ID 15 v.

9741 Gurbak-

9741 GENBANK 11639
(AF086835)



NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

Score = 2890 bits (1503), Expect = 0.0
Identities = 1686/1768 (95%), Gaps = 1/1768 (0%)
Strand=Plus/Plus

Query	1	ACCAGCGCACTTCGGCAGCGGCAGCACCTCGGCAGCACCTCAGCAGCAACATGCCAGCA	60
Sbjct	1	ACCAGCGCACTTCGGCAGCGGCAGCACCTCGGCAGCACCTCAGCAGCAACATGCCAGCA	60
Query	61	AGAAGAATGGAAGAAGCGGACCCCAACCCATAAAAGGTGGGTGTTCACCTCTGAATAATC	120
Sbjct	61	AGAAGAATGGAAGAAGCGGACCCCAACCACATAAAAGGTGGGTGTTCACGCTGAATAATC	120
Query	121	CTTCCGAAGACGAGCGCAAGAAAATACGGGATCTTCCAATATCCCTATTGATTATTTTA	180
Sbjct	121	CTTCCGAAAACAAGCGCAAGAAAATACGGGAGCTCCCAATCTCCCTATTGATTATTTTA	180

1

Query	181	TTGTTGGCGAGGAGGGTAATGAGGAAGGACGAACACCTCACCTCCAGGGGTTGCTAATT	240
Sbjct	181	TTGTTGGCGAGGAGGGTAATGAGGAAGGACGAACACCTCACCTCCAGGGGTTGCTAATT	240
Query	241	TTGTGAAGAAGCAGACTTTTAATAAAGTGAAGTGGTATTTGGGTGCCCCTGCCACATCG	300
Sbjct	241	TTGTGAAGAAGCAAACCTTTTAATAAAGTGAAGTGGTATTTGGGTGCCCCTGCCACATCG	300
Query	301	AGAAAGCGAAAGGAACAGATCAGCAGAATAAAGAATACTGCAGTAAAGAAGGCAACTTAC	360
Sbjct	301	AGAAAGCCAAAGGAACCTGATCAGCAAAATAAAGAATATTGCAGTAAAGAAGGCAACTTAC	360
Query	361	TGATGGAGTGTGGAGCTCCTAGATCTCAGGGACAACGGAGTGACCTGTCTACTGCTGTGA	420
Sbjct	361	TTATTGAATGTGGAGCTCCTCGATCTCAAGGACAACGGAGTGACCTGTCTACTGCTGTGA	420
Query	421	GTACCTTGTGGAGAGCGGGAGTCTGGTGACCGTTGCAGAGCAGCACCTGTAACGTTTG	480
Sbjct	421	GTACCTTGTGGAGAGCGGGATTCTGGTGACCGTTGCAAAGCAGCACCTGTAACGTTTG	480
Query	481	TCAGAAATTTCCGCGGGCTGGCTGAACTTTTGAAAGTGAGCGGGAAAATGCAGAAGCGTG	540
Sbjct	481	TCAAAATTTCCGCGGGCTGGCTGAACTTTTGAAAGTGAGCGGGAAAATGCAAAGCGTG	540
Query	541	ATTGGAAGACTAATGTACACGTCATTGTGGGGCCACCTGGGTGTGGTAAAAGCAAATGGG	600
Sbjct	541	ATTGGAAGAACCAATGTACACTTCATTGTGGGGCCACCTGGGTGTGGTAAAAGCAAATGGG	600
Query	601	CTGCTAATTTTGCAGACCCGGAACACATACTGGAAACCACCTAGAAAACAAGTGGTGGG	660
Sbjct	601	CTGCTAATTTTGCAAACCCGGAACACATACTGGAAACCACCTAAAACAAGTGGTGGG	660
Query	661	ATGGTTACCATGGTGAAGAAGTGGTTGTATTGATGACTTTTATGGCTGGCTGCCCTGGG	720
Sbjct	661	ATGGTTACCATGGTGAAGAAGTGGTTGTATTGATGACTTTTATGGCTGGCTGCCCTGGG	720
Query	721	ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAGAGACTAAAGGTGGAAGT	780
Sbjct	721	ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAAAACTAAAGGTGGAAGT	780
Query	781	TACCTTTTTTGGCCCGCAGTATTCTGATTACCAGCAATCAGACCCCGTTGGAATGGTACT	840
Sbjct	781	TACCTTTTTTGGCCCGCAGTATTCTGATTACCAGCAATCAGACCCCGTTGGAATGGTACT	840
Query	841	CCTCAACTGCTGTCCCAGCTGTAGAAGCTCTTATCGGAGGATTACTTCCTTGGTATTTT	900
Sbjct	841	CCTCAACTGCTGTCCCAGCTGTAGAAGCTCTATCGGAGGATTACTTCCTTGGTATTTT	900
Query	901	GGAAGAAATGCTACAGAACAATCCACGGAGGAAGGGGGCCAGTTTCGTCACCCTTTnnnnnn	960
Sbjct	901	GGAAGAAATGCTACAGAACAATCCACGGAGGAAGGGGGCCAGTTTGTACCCCTTTCCCCC	960
Query	961	nATGCCCTGAATTTCCATATGAAATAAATTACTGAGTCTTTTTTATCACTTCGTAATGGT	1020
Sbjct	961	CATGCCCTGAATTTCCATATGAAATAAATTACTGAGTCTTTTTTATCACTTCGTAATGGT	1020
Query	1021	TTTTATTATTCATTAAGGG-TTAAGTGGGGGCTTTAAAATTAAATTCTCTGAATTGTA	1079
Sbjct	1021	TTTTATTATTCATTTAGGGTTTAAGTGGGGGCTTTAAGATTAAATTCTCTGAATTGTA	1080

Blast Result

Page 3 of 4

```

Query  1080  CATACATGGTTACACGGATATTGTATTCCTGGTCGTATATACTGTTTTCGAACGCAGTGC  1139
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1081  CATACATGGTTACACGGATATTGTAGTCCTGGTCGTATTTACTGTTTTCGAACGCAGTGC  1140

Query  1140  CGAGGCCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTTCTTT  1199
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1141  CGAGGCCTACGTGGTCCACATTTCCAGAGGTTTGTAGCCTCAGCCAAAGCTGATTCTTT  1200

Query  1200  TGTGTGTTGGTTGGAAGTAATCAATAGTGAAATCTAGGACAGGTTTGGGGGTAAAGTACC  1259
          ||||| |||||||||||||||||||||||||||| || |||||||||||||||| || |||||
Sbjct  1201  TGTATTGTTGGTTGGAAGTAATCAATAGTGGAGTCAAGAACAGGTTTGGGTGTGAAGTAAC  1260

Query  1260  GGGAGTGGTAGGAGAAGGGCTGGGTTATGGTATGGCGGGAGGAGTAGTTACATAGGGGT  1319
          |||||||||||||||||| |||| || |||||||||||||||||||||||||||| |||||
Sbjct  1261  GGGAGTGGTAGGAGAAGGGTGGGGGATTGTATGGCGGGAGGAGTAGTTACATATGGGT  1320

Query  1320  CATAGGTGAGGGCTGTGGCCTTTGTTACAAAGTTATCATCTAAAATAACAGCACTGGAGC  1379
          ||||||| |||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  1321  CATAGGTGAGGGCTGTGGCCTTTGTTACAAAGTTATCATCTAAAATAACAGCAGTGGAGC  1380

Query  1380  CCACTCCCTGTCAACCCTGGGTGATCGGGGAGCAGGGCCAGAATTC AACCTTAACCTTTC  1439
          ||||||||||| |||||||||||||||||| |||||||||||||||||||||||||||| |||||||
Sbjct  1381  CCACTCCCTATCAACCCTGGGTGATGGGGGAGCAGGGCCAGAATTC AACCTTAACCTTTC  1440

Query  1440  TTATTCTGTAGTATTCAAAGGGCACAGAGCGGGGGTTTGACCCCCCTCCTGGGGGAAGAA  1499
          |||||||||||||||||||| || |||| || || |||||||| || ||||| ||
Sbjct  1441  TTATTCTGTAGTATTCAAAGGGTATAGAGATTTTGTTGGTCCCCCTCCCGGGGAACAA  1500

Query  1500  AGTCATTAATATTGAATCTCATCATGTCCACCGCCAGGAGGGCGTTCTGACTGTGGTTC  1559
          ||||| || |||| || |||||||||||||||||||||||||||||||||||| ||||||||| ||
Sbjct  1501  AGTCGTCAATTTTAAATCTCATCATGTCCACCGCCAGGAGGGCGTTGTGACTGTGGTAC  1560

Query  1560  GCTTGACAGTATATCCGAAGGTGCGGGAGAGGCGGGTGTTGAAGATGCCATTTTTCCTTC  1619
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1561  GCTTGACAGTATATCCGAAGGTGCGGGAGAGGCGGGTGTTGAAGATGCCATTTTTCCTTC  1620

Query  1620  TCCAGCGGTAACGGTGGCGGGGGTGGACGAGCCAGGGGCGGCGGCGGAGGATCTGGCCAA  1679
          ||||| ||||||| |||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  1621  TCCAACGGTAGCGGTGGCGGGGGTGGACGAGCCAGGGGCGGCGGCGGAGGATCTGGCCAA  1680

Query  1680  GATGGCTGCGGGGGCGGTGTCTTCTTCTCGGTAACGCCTCCTTGGATACGTCATATCTG  1739
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1681  GATGGCTGCGGGGGCGGTGTCTTCTTCTCGGTAACGCCTCCTTGGATACGTCATAGCTG  1740

Query  1740  AAAACGAAAGAAGTGCCTGTAAGTATT  1767
          ||||||||||||||||||
Sbjct  1741  AAAACGAAAGAAGTGCCTGTAAGTATT  1768

```

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total secs.

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

1
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 360
Number of extensions: 6
Number of successful extensions: 4
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 1767
Length of database: 16,974,423,555
Length adjustment: 27
Effective length of query: 1740
Effective length of database: 16,974,423,528
Effective search space: 29535496938720
Effective search space used: 29535496938720
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 14 (27.6 bits)
S2: 22 (43.0 bits)



Structure

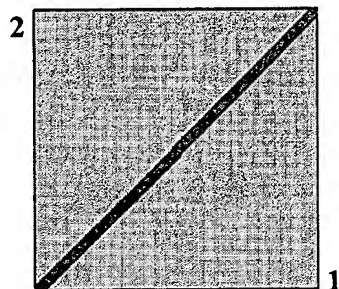
Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ View option
 Masking character option Masking color option
☐ Show CDS translation

Sequence 2: lcl|seq_2
Length = 1768 (1 .. 1768)

Q741 Figure

Verify

97418 FIGURE 1639
97418 PTO 1639



NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

Score = 3355 bits (1745), Expect = 0.0
Identities = 1765/1768 (99%), Gaps = 0/1768 (0%)
Strand=Plus/Plus

Query	1	ACCAGCGCACTTCGGCAGCGGCAGCACCTCGGCAGCACCTCAGCAGCAACATGCCCAGCA	60
Sbjct	1	ACCAGCGCACTTCGGCAGCGGCAGCACCTCGGCAGCACCTCAGCAGCAACATGCCCAGCA	60
Query	61	AGAAGAATGGAAGAAGCGGACCCCAACCACATAAAAGGTGGGTGTTACGCTGAATAATC	120
Sbjct	61	AGAAGAATGGAAGAAGCGGACCCCAACCACATAAAAGGTGGGTGTTACGCTGAATAATC	120
Query	121	CTTCCGAAGACAAGCGCAAGAAAATACGGGAGCTCCCAATCTCCCTATTTGATTATTTTA	180
Sbjct	121	CTTCCGAAGACAAGCGCAAGAAAATACGGGAGCTCCCAATCTCCCTATTTGATTATTTTA	180

```
Query 181 TTGTTGGCGAGGAGGGTAATGAGGAAGGACGAACACCTCACCTCCAGGGGTTTCGCTAATT 240
|||||
Sbjct 181 TTGTTGGCGAGGAGGGTAATGAGGAAGGACGAACACCTCACCTCCAGGGGTTTCGCTAATT 240

Query 241 TTGTGAAGAAGCAAACCTTTTAATAAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG 300
|||||
Sbjct 241 TTGTGAAGAAGCAAACCTTTTAATAAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG 300

Query 301 AGAAAGCCAAAGGAAGTATCAGCAAAATAAAGAATATTGCAGTAAAGAAGGCAACTTAC 360
|||||
Sbjct 301 AGAAAGCCAAAGGAAGTATCAGCAGAAATAAAGAATATTGCAGTAAAGAAGGCAACTTAC 360

Query 361 TTATTGAATGTGGAGCTCCTCGATCTCAAGGACAACGGAGCGACCTGTCTACTGCTGTGA 420
|||||
Sbjct 361 TTATTGAATGTGGAGCTCCTCGATCTCAAGGACAACGGAGTGACCTGTCTACTGCTGTGA 420

Query 421 GTACCTTGTGGAGAGCGGGATTCTGGTGACCGTTGCAAAGCAGCACCTGTAACGTTTG 480
|||||
Sbjct 421 GTACCTTGTGGAGAGCGGGATTCTGGTGACCGTTGCAAAGCAGCACCTGTAACGTTTG 480

Query 481 TCAAAAATTTCCGCGGGCTGGCTGAACCTTTTGAAGTGAGCGGGAAAATGCAAAGCGTG 540
|||||
Sbjct 481 TCAAAAATTTCCGCGGGCTGGCTGAACCTTTTGAAGTGAGCGGGAAAATGCAAAGCGTG 540

Query 541 ATTGGAAAACCAATGTACACTTCATTGTGGGGCCACCTGGGTGTGGTAAAAGCAAATGGG 600
|||||
Sbjct 541 ATTGGAAAACCAATGTACACTTCATTGTGGGGCCACCTGGGTGTGGTAAAAGCAAATGGG 600

Query 601 CTGCTAATTTTGCAAACCCGGAACACATACTGGAACACCTAAAAACAAGTGGTGGG 660
|||||
Sbjct 601 CTGCTAATTTTGCAAACCCGGAACACATACTGGAACACCTAAAAACAAGTGGTGGG 660

Query 661 ATGGTTACCATGGTGAAAAAGTGGTTGTTATTGATGACTTTTATGGCTGGCTGCCGTGGG 720
|||||
Sbjct 661 ATGGTTACCATGGTGAAAAAGTGGTTGTTATTGATGACTTTTATGGCTGGCTGCCGTGGG 720

Query 721 ATGATCTACTGAAACTGTGTGATCGATATCCATTGACTGTAAAAACTAAAGGTGGAAGT 780
|||||
Sbjct 721 ATGATCTACTGAAACTGTGTGATCGATATCCATTGACTGTAAAAACTAAAGGTGGAAGT 780

Query 781 TACCTTTTTTGGCCCGCAGTATTCTGATTACCAGCAATCAGACCCCGTTGGAATGGTACT 840
|||||
Sbjct 781 TACCTTTTTTGGCCCGCAGTATTCTGATTACCAGCAATCAGACCCCGTTGGAATGGTACT 840

Query 841 CCTCAACTGCTGTCCAGCTGTAGAAGCTCTCTATCGGAGGATTACTTCCTTGGTATTTT 900
|||||
Sbjct 841 CCTCAACTGCTGTCCAGCTGTAGAAGCTCTCTATCGGAGGATTACTTCCTTGGTATTTT 900

Query 901 GGAAGAATGCTACAAAACAATCCACGGAGGAAGGGGGCCAGTTTGTACCCTTTnnnnnn 960
|||||
Sbjct 901 GGAAGAATGCTACAGAAACAATCCACGGAGGAAGGGGGCCAGTTTGTACCCTTTCCCCC 960

Query 961 nATGCCCTGAATTTCCATATGAAATAAATTACTGAGTCTTTTTTATCACTTCGTAATGGT 1020
|||||
Sbjct 961 CATGCCCTGAATTTCCATATGAAATAAATTACTGAGTCTTTTTTATCACTTCGTAATGGT 1020

Query 1021 TTTTATTATTCATTTAGGGTTTAAGTGGGGGGTCTTTAAGATTAAATTCTCTGAATTGTA 1080
|||||
Sbjct 1021 TTTTATTATTCATTTAGGGTTTAAGTGGGGGGTCTTTAAGATTAAATTCTCTGAATTGTA 1080
```

Blast Result

Page 3 of 4

Query 1081 CATACATGGTTACACGGATATTGTAGTCCTGGTCGTATTTACTGTTTTCGAACGCAGTGC 1140
|||||
Sbjct 1081 CATACATGGTTACACGGATATTGTAGTCCTGGTCGTATTTACTGTTTTCGAACGCAGTGC 1140

Query 1141 CGAGGCCTACGTGGTCCACATTTCCAGAGGTTTGTAGCCTCAGCCAAAGCTGATTCCTTT 1200
|||||
Sbjct 1141 CGAGGCCTACGTGGTCCACATTTCCAGAGGTTTGTAGCCTCAGCCAAAGCTGATTCCTTT 1200

Query 1201 TGTTATTTGGTTGGAAGTAATCAATAGTGGAGTCAAGAACAGGTTTGGGTGTGAAGTAAC 1260
|||||
Sbjct 1201 TGTTATTTGGTTGGAAGTAATCAATAGTGGAGTCAAGAACAGGTTTGGGTGTGAAGTAAC 1260

Query 1261 GGGAGTGGTAGGAGAAGGGTTGGGGGATTGTATGGCGGGAGGAGTAGTTTACATATGGGT 1320
|||||
Sbjct 1261 GGGAGTGGTAGGAGAAGGGTTGGGGGATTGTATGGCGGGAGGAGTAGTTTACATATGGGT 1320

Query 1321 CATAGGTTAGGGCTGTGGCCTTTGTTACAAAGTTATCATCTAAAATAACAGCAGTGGAGC 1380
|||||
Sbjct 1321 CATAGGTTAGGGCTGTGGCCTTTGTTACAAAGTTATCATCTAAAATAACAGCAGTGGAGC 1380

Query 1381 CCACTCCCCTATCACCCTGGGTGATGGGGGAGCAGGGCCAGAATTCAACCTTAACCTTTC 1440
|||||
Sbjct 1381 CCACTCCCCTATCACCCTGGGTGATGGGGGAGCAGGGCCAGAATTCAACCTTAACCTTTC 1440

Query 1441 TTATTCTGTAGTATTCAAAGGGTATAGAGATTTTGTGGTCCCCCTCCCGGGGAACAA 1500
|||||
Sbjct 1441 TTATTCTGTAGTATTCAAAGGGTATAGAGATTTTGTGGTCCCCCTCCCGGGGAACAA 1500

Query 1501 AGTCGTCAATTTTAAATCTCATCATGTCCACCGCCCAGGAGGGCGTTGTGACTGTGGTAC 1560
|||||
Sbjct 1501 AGTCGTCAATTTTAAATCTCATCATGTCCACCGCCCAGGAGGGCGTTGTGACTGTGGTAC 1560

Query 1561 GCTTGACAGTATATCCGAAGGTGCGGGAGAGGCGGGTGTGAAGATGCCATTTTTCCTTC 1620
|||||
Sbjct 1561 GCTTGACAGTATATCCGAAGGTGCGGGAGAGGCGGGTGTGAAGATGCCATTTTTCCTTC 1620

Query 1621 TCCAACGGTAGCGGTGGCGGGGTGGACGAGCCAGGGGCGGCGGCGGAGGATCTGGCCAA 1680
|||||
Sbjct 1621 TCCAACGGTAGCGGTGGCGGGGTGGACGAGCCAGGGGCGGCGGCGGAGGATCTGGCCAA 1680

Query 1681 GATGGCTGCGGGGGCGGTGTCTTCTTCTGCGGTAACGCCTCCTTGATACGTCATAGCTG 1740
|||||
Sbjct 1681 GATGGCTGCGGGGGCGGTGTCTTCTTCTGCGGTAACGCCTCCTTGATACGTCATAGCTG 1740

Query 1741 AAAACGAAAGAAGTGCCTGTAAGTATT 1768
|||||
Sbjct 1741 AAAACGAAAGAAGTGCCTGTAAGTATT 1768

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda K H
1.33 0.621 1.12Gapped
Lambda K H
1.33 0.621 1.12

Blast Result

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 470
Number of extensions: 5
Number of successful extensions: 3
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 1768
Length of database: 16,974,423,555
Length adjustment: 27
Effective length of query: 1741
Effective length of database: 16,974,423,528
Effective search space: 29552471362248
Effective search space used: 29552471362248
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 14 (27.6 bits)
S2: 22 (43.0 bits)

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